

SEQUENCE LISTING

<110> MATSUZAWA, Yuji
 FUNAHASHI, Toru
 SHIMOMURA, Ichirou
 FURUYAMA, Naoki

<120> Novel Proteins and Use Thereof

<130> 3083US0P

<150> PCT/JP03/08690

<151> 2003-07-09

<150> JP 2002-201856

<151> 2002-07-10

<160> 48

<170> PatentIn version 3.1

<210> 1

<211> 1836

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1833)

<223>

<220>

<221> sig_peptide

<222> (1)..(69)

<223>

<220>

<221> mat_peptide

<222> (70)..()

<223>

<220>

<221> misc_feature

<222> (798)..(798)

<223> 'n' stands for unidentified base.

<400> 1

atg gct ggc agc agg ggc ctg cca ctc cta ctg ctg gtg ctt cag ctc 48
 Met Ala Gly Ser Arg Gly Leu Pro Leu Leu Leu Leu Val Leu Gln Leu
 -20 -15 -10

ttc ctg ggc cct gtg ctg cct gtg agg gca cct gtg ttt ggc cga agt 96
 Phe Leu Gly Pro Val Leu Pro Val Arg Ala Pro Val Phe Gly Arg Ser
 -5 -1 1 5

gac acc ccc acc ctg agc ccc gag gag aat gaa ttt gtg gag gaa gag 144

Asp Thr Pro Thr Leu Ser Pro Glu Glu Asn Glu Phe Val Glu Glu Glu	
10 15 20 25	
aat cag cca gtg ctg gtt ctg agc tcc gag gag cca gag cct ggc cca	192
Asn Gln Pro Val Leu Val Leu Ser Ser Glu Glu Pro Glu Pro Gly Pro	
30 35 40	
gcc act gtc gac tgt ccc cga gat tgt gcc tgt tcc cag gaa ggt gta	240
Ala Thr Val Asp Cys Pro Arg Asp Cys Ala Cys Ser Gln Glu Gly Val	
45 50 55	
gtg gac tgt ggt ggc att gac ctg cgt gag ttt cca ggc gac ctg ccc	288
Val Asp Cys Gly Gly Ile Asp Leu Arg Glu Phe Pro Gly Asp Leu Pro	
60 65 70	
gag cac acc aac cat ctc tcc ttg cag aac aac cag ctg gag aag atc	336
Glu His Thr Asn His Leu Ser Leu Gln Asn Asn Gln Leu Glu Lys Ile	
75 80 85	
tac ccc gag gag ctg tcc cgg ctg cag cgg ctg gag acg ctg aac ctg	384
Tyr Pro Glu Glu Leu Ser Arg Leu Gln Arg Leu Glu Thr Leu Asn Leu	
90 95 100 105	
cag aac aac cgc ctg aca tcc cga ggg ctc cca gag gag gca ttt gag	432
Gln Asn Asn Arg Leu Thr Ser Arg Gly Leu Pro Glu Glu Ala Phe Glu	
110 115 120	
cat ctt act agc ctc aat tac ctg tac ctg gcc aac aac aag ctg aca	480
His Leu Thr Ser Leu Asn Tyr Leu Tyr Leu Ala Asn Asn Lys Leu Thr	
125 130 135	
ctg gca ccc cga ttc ctg cca aac gcc ctg atc agt gtg gac ttt gct	528
Leu Ala Pro Arg Phe Leu Pro Asn Ala Leu Ile Ser Val Asp Phe Ala	
140 145 150	
gcc aat tat ctc act aag atc tat gga ctc acc ttt ggc caa aag cca	576
Ala Asn Tyr Leu Thr Lys Ile Tyr Gly Leu Thr Phe Gly Gln Lys Pro	
155 160 165	
aat ctg agg tct gtg tac ctg cat aac aac aag cta gca gat gcc ggg	624
Asn Leu Arg Ser Val Tyr Leu His Asn Asn Lys Leu Ala Asp Ala Gly	
170 175 180 185	
ctg ccg gac cac atg ttc aat ggc tcc agc aac gtc gag atc cta atc	672
Leu Pro Asp His Met Phe Asn Gly Ser Ser Asn Val Glu Ile Leu Ile	
190 195 200	
ctg tcc agc aac ttc ctg cgc cat gtg ccc aag cac ctg cca ccc gct	720
Leu Ser Ser Asn Phe Leu Arg His Val Pro Lys His Leu Pro Pro Ala	
205 210 215	
ctg tac aag ctg cac ctc aag aac aat aag cta gag aag atc ccc cct	768
Leu Tyr Lys Leu His Leu Lys Asn Asn Lys Leu Glu Lys Ile Pro Pro	
220 225 230	
ggg gcc ttc agt gag ctg agc aac cta cgn gaa ctc tac ctg cag aac	816
Gly Ala Phe Ser Glu Leu Ser Asn Leu Arg Glu Leu Tyr Leu Gln Asn	

235	240	245	
aac tac ctg acc gac gag ggt ctg gac aac gag acc ttc tgg aag ctg Asn Tyr Leu Thr Asp Glu Gly Leu Asp Asn Glu Thr Phe Trp Lys Leu 250 255 260 265			864
tcc agc ctg gag tac ctg gac ttg tcc agc acc aac ctg tcg agg gtc Ser Ser Leu Glu Tyr Leu Asp Leu Ser Ser Thr Asn Leu Ser Arg Val 270 275 280			912
cca gcg ggt ctt ccc cgc agc ctg gtc ctg ctg cac ctg gag aaa aat Pro Ala Gly Leu Pro Arg Ser Leu Val Leu Leu His Leu Glu Lys Asn 285 290 295			960
gcc atc cag agc gta gaa gct gat gtg ctg aca ccc atc cgc aac ctg Ala Ile Gln Ser Val Glu Ala Asp Val Leu Thr Pro Ile Arg Asn Leu 300 305 310			1008
gag tac ctg ctg cta cat agc aac cag ctg cag gcc aag ggt atc cac Glu Tyr Leu Leu Leu His Ser Asn Gln Leu Gln Ala Lys Gly Ile His 315 320 325			1056
cca ctg gcc ttc cag ggc ctc aag aag ctc cac aca gtg cat cta tac Pro Leu Ala Phe Gln Gly Leu Lys Lys Leu His Thr Val His Leu Tyr 330 335 340 345			1104
aac aac gcg ctg gaa cgt gtg ccc agc ggc ctg ccc cgc cga gtg cgc Asn Asn Ala Leu Glu Arg Val Pro Ser Gly Leu Pro Arg Arg Val Arg 350 355 360			1152
acc ctc atg atc ctg cac aac cag att aca ggc ata ggc cgt gag gac Thr Leu Met Ile Leu His Asn Gln Ile Thr Gly Ile Gly Arg Glu Asp 365 370 375			1200
ttc gct acc acc tac ttc ctg gaa gag ctc aac ctc agc tac aac cgc Phe Ala Thr Thr Tyr Phe Leu Glu Glu Leu Asn Leu Ser Tyr Asn Arg 380 385 390			1248
atc acc agc cca cag atg cac cga gat gcc ttc cgc aag cta cgc ctg Ile Thr Ser Pro Gln Met His Arg Asp Ala Phe Arg Lys Leu Arg Leu 395 400 405			1296
ctg cgt tca ctt gac ttg tct ggc aac cgt ctg caa aca ctg cct cca Leu Arg Ser Leu Asp Leu Ser Gly Asn Arg Leu Gln Thr Leu Pro Pro 410 415 420 425			1344
ggc ctg ccg aaa aac gta cac gtg ctc aag gtc aag cgg aat gag ctg Gly Leu Pro Lys Asn Val His Val Leu Lys Val Lys Arg Asn Glu Leu 430 435 440			1392
gct gcc ctg gca cgt ggg gca cta gct ggc atg gcc cag ctt cgg gaa Ala Ala Leu Ala Arg Gly Ala Leu Ala Gly Met Ala Gln Leu Arg Glu 445 450 455			1440
ctc tac ctc aca ggc aac cga ctg cga agc cgg gcc ctg gga ccc cgt Leu Tyr Leu Thr Gly Asn Arg Leu Arg Ser Arg Ala Leu Gly Pro Arg 460 465 470			1488

gcc tgg gtg gac ctt gct ggt ctg cag ctg ctg gac atc gct ggg aat	1536
Ala Trp Val Asp Leu Ala Gly Leu Gln Leu Leu Asp Ile Ala Gly Asn	
475 480 485	
cag ctc aca gag gtc cct gag ggg ctc ccc cca tct ctg gag tat ctg	1584
Gln Leu Thr Glu Val Pro Glu Gly Leu Pro Pro Ser Leu Glu Tyr Leu	
490 495 500 505	
tac ctg cag aat aac aag att agt gcc gtt cct gcc aac gcc ttt gac	1632
Tyr Leu Gln Asn Asn Lys Ile Ser Ala Val Pro Ala Asn Ala Phe Asp	
510 515 520	
tcc act ccc aac ctt aag ggg atc ttt ctc agg ttc aac aag ctg gct	1680
Ser Thr Pro Asn Leu Lys Gly Ile Phe Leu Arg Phe Asn Lys Leu Ala	
525 530 535	
gtg ggc tcc gtg gtg gaa agc gcc ttc cgg agg ctg aaa cac ctg cag	1728
Val Gly Ser Val Val Glu Ser Ala Phe Arg Arg Leu Lys His Leu Gln	
540 545 550	
gtc ttg gac att gaa ggc aac ttt gag ttt ggt aat ggt tcc aag gac	1776
Val Leu Asp Ile Glu Gly Asn Phe Glu Phe Gly Asn Gly Ser Lys Asp	
555 560 565	
aaa gat gag gaa gag gaa gaa gag gag gaa gag gaa gat gag gaa gag	1824
Lys Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu	
570 575 580 585	
gaa act aga tag	1836
Glu Thr Arg	

<210> 2
 <211> 611
 <212> PRT
 <213> Mus musculus

<400> 2

Met Ala Gly Ser Arg Gly Leu Pro Leu Leu Leu Leu Val Leu Gln Leu
-20 -15 -10

Phe Leu Gly Pro Val Leu Pro Val Arg Ala Pro Val Phe Gly Arg Ser
-5 -1 1 5

Asp Thr Pro Thr Leu Ser Pro Glu Glu Asn Glu Phe Val Glu Glu Glu
10 15 20 25

Asn Gln Pro Val Leu Val Leu Ser Ser Glu Glu Pro Glu Pro Gly Pro
30 35 40

Ala Thr Val Asp Cys Pro Arg Asp Cys Ala Cys Ser Gln Glu Gly Val
 45 50 55

Val Asp Cys Gly Gly Ile Asp Leu Arg Glu Phe Pro Gly Asp Leu Pro
 60 65 70

Glu His Thr Asn His Leu Ser Leu Gln Asn Asn Gln Leu Glu Lys Ile
 75 80 85

Tyr Pro Glu Glu Leu Ser Arg Leu Gln Arg Leu Glu Thr Leu Asn Leu
 90 95 100 105

Gln Asn Asn Arg Leu Thr Ser Arg Gly Leu Pro Glu Glu Ala Phe Glu
 110 115 120

His Leu Thr Ser Leu Asn Tyr Leu Tyr Leu Ala Asn Asn Lys Leu Thr
 125 130 135

Leu Ala Pro Arg Phe Leu Pro Asn Ala Leu Ile Ser Val Asp Phe Ala
 140 145 150

Ala Asn Tyr Leu Thr Lys Ile Tyr Gly Leu Thr Phe Gly Gln Lys Pro
 155 160 165

Asn Leu Arg Ser Val Tyr Leu His Asn Asn Lys Leu Ala Asp Ala Gly
 170 175 180 185

Leu Pro Asp His Met Phe Asn Gly Ser Ser Asn Val Glu Ile Leu Ile
 190 195 200

Leu Ser Ser Asn Phe Leu Arg His Val Pro Lys His Leu Pro Pro Ala
 205 210 215

Leu Tyr Lys Leu His Leu Lys Asn Asn Lys Leu Glu Lys Ile Pro Pro
 220 225 230

Gly Ala Phe Ser Glu Leu Ser Asn Leu Arg Glu Leu Tyr Leu Gln Asn
 235 240 245

Asn Tyr Leu Thr Asp Glu Gly Leu Asp Asn Glu Thr Phe Trp Lys Leu
 250 255 260 265

Ser Ser Leu Glu Tyr Leu Asp Leu Ser Ser Thr Asn Leu Ser Arg Val

270	275	280
Pro Ala Gly Leu Pro Arg Ser Leu Val Leu Leu His Leu Glu Lys Asn		
285	290	295
Ala Ile Gln Ser Val Glu Ala Asp Val Leu Thr Pro Ile Arg Asn Leu		
300	305	310
Glu Tyr Leu Leu Leu His Ser Asn Gln Leu Gln Ala Lys Gly Ile His		
315	320	325
Pro Leu Ala Phe Gln Gly Leu Lys Lys Leu His Thr Val His Leu Tyr		
330	335	340
Asn Asn Ala Leu Glu Arg Val Pro Ser Gly Leu Pro Arg Arg Val Arg		
350	355	360
Thr Leu Met Ile Leu His Asn Gln Ile Thr Gly Ile Gly Arg Glu Asp		
365	370	375
Phe Ala Thr Thr Tyr Phe Leu Glu Glu Leu Asn Leu Ser Tyr Asn Arg		
380	385	390
Ile Thr Ser Pro Gln Met His Arg Asp Ala Phe Arg Lys Leu Arg Leu		
395	400	405
Leu Arg Ser Leu Asp Leu Ser Gly Asn Arg Leu Gln Thr Leu Pro Pro		
410	415	420
Gly Leu Pro Lys Asn Val His Val Leu Lys Val Lys Arg Asn Glu Leu		
430	435	440
Ala Ala Leu Ala Arg Gly Ala Leu Ala Gly Met Ala Gln Leu Arg Glu		
445	450	455
Leu Tyr Leu Thr Gly Asn Arg Leu Arg Ser Arg Ala Leu Gly Pro Arg		
460	465	470
Ala Trp Val Asp Leu Ala Gly Leu Gln Leu Leu Asp Ile Ala Gly Asn		
475	480	485
Gln Leu Thr Glu Val Pro Glu Gly Leu Pro Pro Ser Leu Glu Tyr Leu		
490	495	500
		505

Tyr Leu Gln Asn Asn Lys Ile Ser Ala Val Pro Ala Asn Ala Phe Asp
510 515 520

Ser Thr Pro Asn Leu Lys Gly Ile Phe Leu Arg Phe Asn Lys Leu Ala
525 530 535

Val Gly Ser Val Val Glu Ser Ala Phe Arg Arg Leu Lys His Leu Gln
540 545 550

Val Leu Asp Ile Glu Gly Asn Phe Glu Phe Gly Asn Gly Ser Lys Asp
555 560 565

Lys Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu
570 575 580 585

Glu Thr Arg

<210> 3
<211> 480
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(477)
<223>

<220>
<221> sig_peptide
<222> (1)..(69)
<223>

<220>
<221> mat_peptide
<222> (70)..()
<223>

<400> 3
atg gct ggc agc agg ggc ctg cca ctc cta ctg ctg gtg ctt cag ctc 48
Met Ala Gly Ser Arg Gly Leu Pro Leu Leu Leu Leu Val Leu Gln Leu
-20 -15 -10

ttc ctg ggc cct gtg ctg cct gtg agg gca cct gtg ttt ggc cga agt 96
Phe Leu Gly Pro Val Leu Pro Val Arg Ala Pro Val Phe Gly Arg Ser
-5 -1 1 5

gac acc ccc acc ctg agc ccc gag gag aat gaa ttt gtg gag gaa gag 144
Asp Thr Pro Thr Leu Ser Pro Glu Glu Asn Glu Phe Val Glu Glu Glu

10	15	20	25	
aat cag cca gtg ctg gtt ctg agc tcc gag gag cca gag cct ggc cca				192
Asn Gln Pro Val Leu Val Leu Ser Ser Glu Glu Pro Glu Pro Gly Pro	30	35	40	
gcc act gtc gac tgt ccc cga gat tgt gcc tgt tcc cag gaa ggt gta				240
Ala Thr Val Asp Cys Pro Arg Asp Cys Ala Cys Ser Gln Glu Gly Val	45	50	55	
gtg gac tgt ggt ggc att gac ctg cgt gag ttt cca ggc gac ctg ccc				288
Val Asp Cys Gly Gly Ile Asp Leu Arg Glu Phe Pro Gly Asp Leu Pro	60	65	70	
gag cac acc aac cat ctc tcc ttg cag aac aac cag ctg gag aag atc				336
Glu His Thr Asn His Leu Ser Leu Gln Asn Asn Gln Leu Glu Lys Ile	75	80	85	
tac ccc gag gag ctg tcc cgg ctg cag cgg ctg gag acg ctg aac ctg				384
Tyr Pro Glu Glu Leu Ser Arg Leu Gln Arg Leu Glu Thr Leu Asn Leu	90	95	100	105
cag aac aac cgc ctg aca tcc cga gct gac act ggc acc ccg att cct				432
Gln Asn Asn Arg Leu Thr Ser Arg Ala Asp Thr Gly Thr Pro Ile Pro	110	115	120	
gcc aaa cgc cct gat cag tgt gga ctt tgc tgc caa tta tct cac taa				480
Ala Lys Arg Pro Asp Gln Cys Gly Leu Cys Cys Gln Leu Ser His	125	130	135	
<210> 4				
<211> 159				
<212> PRT				
<213> Mus musculus				
<400> 4				
Met Ala Gly Ser Arg Gly Leu Pro Leu Leu Leu Leu Val Leu Gln Leu	-20	-15	-10	
Phe Leu Gly Pro Val Leu Pro Val Arg Ala Pro Val Phe Gly Arg Ser	-5	-1 1	5	
Asp Thr Pro Thr Leu Ser Pro Glu Glu Asn Glu Phe Val Glu Glu Glu	10	15	20	25
Asn Gln Pro Val Leu Val Leu Ser Ser Glu Glu Pro Glu Pro Gly Pro	30	35	40	
Ala Thr Val Asp Cys Pro Arg Asp Cys Ala Cys Ser Gln Glu Gly Val	45	50	55	

Val Asp Cys Gly Gly Ile Asp Leu Arg Glu Phe Pro Gly Asp Leu Pro
60 65 70

Glu His Thr Asn His Leu Ser Leu Gln Asn Asn Gln Leu Glu Lys Ile
75 80 85

Tyr Pro Glu Glu Leu Ser Arg Leu Gln Arg Leu Glu Thr Leu Asn Leu
90 95 100 105

Gln Asn Asn Arg Leu Thr Ser Arg Ala Asp Thr Gly Thr Pro Ile Pro
110 115 120

Ala Lys Arg Pro Asp Gln Cys Gly Leu Cys Cys Gln Leu Ser His
125 130 135

<210> 5
<211> 1092
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(1089)
<223>

<220>
<221> sig_peptide
<222> (1)..(180)
<223>

<220>
<221> mat_peptide
<222> (181)..()
<223>

<400> 5
atg gtg ggt tcc tgt ggt cgc tgc gca gcg gct ggc cga ctt ccg cag 48
Met Val Gly Ser Cys Gly Arg Cys Ala Ala Ala Gly Arg Leu Pro Gln
-60 -55 -50 -45

cgg gtc tcg ggc cac cga gcg ccg tct tca ccc agc gcc atg gct gtg 96
Arg Val Ser Gly His Arg Ala Pro Ser Ser Pro Ser Ala Met Ala Val
-40 -35 -30

gcc gct gtc ggc cgc ccg aga gcc ctg cgc tgc ccg ctg ttg ctc ctg 144
Ala Ala Val Gly Arg Pro Arg Ala Leu Arg Cys Pro Leu Leu Leu Leu
-25 -20 -15

ctg tca ctc ctg ctg gta gcc ggc cct gcg ctg ggc tgg aac gac cct 192
Leu Ser Leu Leu Leu Val Ala Gly Pro Ala Leu Gly Trp Asn Asp Pro
-10 -5 -1 1

gac aga ata ctc ttg cgg gat gtg aaa gct ctt acc ctc tac tcc gac Asp Arg Ile Leu Leu Arg Asp Val Lys Ala Leu Thr Leu Tyr Ser Asp 5 10 15 20	240
cgc tac acc acc tcc cgg agg ctg gac cct atc cca cag ttg aag tgt Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys Cys 25 30 35	288
gtt gga ggc acc gcc ggt tgt gag gcc tat acc ccc agg gtg ata cag Val Gly Gly Thr Ala Gly Cys Glu Ala Tyr Thr Pro Arg Val Ile Gln 40 45 50	336
tgc cag aac aaa ggc tgg gat ggc tac gat gta cag tgg gaa tgt aag Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys Lys 55 60 65	384
acc gac ttg gat att gca tac aaa ttt ggc aaa act gtg gtg agc tgt Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser Cys 70 75 80	432
gaa ggc tac gag tcc tct gaa gac cag tat gtc ctc agg ggt tcc tgc Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser Cys 85 90 95 100	480
ggc ttg gag tac aac tta gat tac aca gag ctg ggc ctg aag aaa ctg Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Lys Lys Leu 105 110 115	528
aag gag tct gga aag cac cag ggc ttc tct gat tat tat cac aag ctg Lys Glu Ser Gly Lys His Gln Gly Phe Ser Asp Tyr Tyr His Lys Leu 120 125 130	576
tgc tcc tca gat tcc tgt ggc ttt att acc att gca gta ctg ttt gtt Cys Ser Ser Asp Ser Cys Gly Phe Ile Thr Ile Ala Val Leu Phe Val 135 140 145	624
ctc gcc ttt gcg gtt tac aag ctg ttc ctc agc gat ggc cag ggg tcg Leu Ala Phe Ala Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Gly Ser 150 155 160	672
cct ccg ccg tat tct gag cac ccg cca tac tca gag cac tct cag agg Pro Pro Pro Tyr Ser Glu His Pro Pro Tyr Ser Glu His Ser Gln Arg 165 170 175 180	720
ttt gcc agt gcc gca ggg gcg cct cct ccg ggc ttt aag tcg gag ttc Phe Ala Ser Ala Ala Gly Ala Pro Pro Pro Gly Phe Lys Ser Glu Phe 185 190 195	768
aca gga cca cag aat act ggc tat ggt gca agc tct ggc ttc ggg agt Thr Gly Pro Gln Asn Thr Gly Tyr Gly Ala Ser Ser Gly Phe Gly Ser 200 205 210	816
gct ttt gga ggc caa ggc tat ggc agt tca ggg ccg ggg ttc tgg tct Ala Phe Gly Gly Gln Gly Tyr Gly Ser Ser Gly Pro Gly Phe Trp Ser 215 220 225	864

ggc ctg gga gct gga gga ctg ctt ggg tat ttg ttt ggc agc aac aga 912
 Gly Leu Gly Ala Gly Gly Leu Leu Gly Tyr Leu Phe Gly Ser Asn Arg
 230 235 240

gcg gcg acg cct ttc tca gac tcg tgg tac cat cca gcc tac cct cct 960
 Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr His Pro Ala Tyr Pro Pro
 245 250 255 260

tcc cac tct ggg gcc tgg aac agt cgg gcc tac tca ccc ctg ggt gga 1008
 Ser His Ser Gly Ala Trp Asn Ser Arg Ala Tyr Ser Pro Leu Gly Gly
 265 270 275

ggc gca ggg agc tat tgt gca tcc tct aat gca gac tcg aga acc aga 1056
 Gly Ala Gly Ser Tyr Cys Ala Ser Ser Asn Ala Asp Ser Arg Thr Arg
 280 285 290

aca gca tca gga tat ggt ggc acc aga aga cgg taa 1092
 Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
 295 300

<210> 6
 <211> 363
 <212> PRT
 <213> Mus musculus

<400> 6

Met Val Gly Ser Cys Gly Arg Cys Ala Ala Ala Gly Arg Leu Pro Gln
 -60 -55 -50 -45

Arg Val Ser Gly His Arg Ala Pro Ser Ser Pro Ser Ala Met Ala Val
 -40 -35 -30

Ala Ala Val Gly Arg Pro Arg Ala Leu Arg Cys Pro Leu Leu Leu Leu
 -25 -20 -15

Leu Ser Leu Leu Leu Val Ala Gly Pro Ala Leu Gly Trp Asn Asp Pro
 -10 -5 -1 1

Asp Arg Ile Leu Leu Arg Asp Val Lys Ala Leu Thr Leu Tyr Ser Asp
 5 10 15 20

Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys Cys
 25 30 35

Val Gly Gly Thr Ala Gly Cys Glu Ala Tyr Thr Pro Arg Val Ile Gln
 40 45 50

Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys Lys

55	60	65
Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser Cys		
70	75	80
Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser Cys		
85	90	95
Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Lys Lys Leu		
	105	110
		115
Lys Glu Ser Gly Lys His Gln Gly Phe Ser Asp Tyr Tyr His Lys Leu		
	120	125
		130
Cys Ser Ser Asp Ser Cys Gly Phe Ile Thr Ile Ala Val Leu Phe Val		
	135	140
		145
Leu Ala Phe Ala Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Gly Ser		
	150	155
		160
Pro Pro Pro Tyr Ser Glu His Pro Pro Tyr Ser Glu His Ser Gln Arg		
165	170	175
		180
Phe Ala Ser Ala Ala Gly Ala Pro Pro Pro Gly Phe Lys Ser Glu Phe		
	185	190
		195
Thr Gly Pro Gln Asn Thr Gly Tyr Gly Ala Ser Ser Gly Phe Gly Ser		
	200	205
		210
Ala Phe Gly Gly Gln Gly Tyr Gly Ser Ser Gly Pro Gly Phe Trp Ser		
	215	220
		225
Gly Leu Gly Ala Gly Gly Leu Leu Gly Tyr Leu Phe Gly Ser Asn Arg		
	230	235
		240
Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr His Pro Ala Tyr Pro Pro		
245	250	255
		260
Ser His Ser Gly Ala Trp Asn Ser Arg Ala Tyr Ser Pro Leu Gly Gly		
	265	270
		275
Gly Ala Gly Ser Tyr Cys Ala Ser Ser Asn Ala Asp Ser Arg Thr Arg		
	280	285
		290

Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
 295 300

<210> 7
 <211> 1005
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(1002)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(93)
 <223>

<220>
 <221> mat_peptide
 <222> (94)..()
 <223>

<400> 7
 atg gct gtg gcc gct gtc ggc cgc ccg aga gcc ctg cgc tgc ccg ctg 48
 Met Ala Val Ala Ala Val Gly Arg Pro Arg Ala Leu Arg Cys Pro Leu
 -30 -25 -20

ttg ctc ctg ctg tca ctc ctg ctg gta gcc ggc cct gcg ctg ggc tgg 96
 Leu Leu Leu Leu Ser Leu Leu Leu Val Ala Gly Pro Ala Leu Gly Trp
 -15 -10 -5 -1 1

aac gac cct gac aga ata ctc ttg cgg gat gtg aaa gct ctt acc ctc 144
 Asn Asp Pro Asp Arg Ile Leu Leu Arg Asp Val Lys Ala Leu Thr Leu
 5 10 15

tac tcc gac cgc tac acc acc tcc cgg agg ctg gac cct atc cca cag 192
 Tyr Ser Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln
 20 25 30

ttg aag tgt gtt gga ggc acc gcc ggt tgt gag gcc tat acc ccc agg 240
 Leu Lys Cys Val Gly Gly Thr Ala Gly Cys Glu Ala Tyr Thr Pro Arg
 35 40 45

gtg ata cag tgc cag aac aaa ggc tgg gat ggc tac gat gta cag tgg 288
 Val Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp
 50 55 60 65

gaa tgt aag acc gac ttg gat att gca tac aaa ttt ggc aaa act gtg 336
 Glu Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val
 70 75 80

gtg agc tgt gaa ggc tac gag tcc tct gaa gac cag tat gtc ctc agg 384
 Val Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg

85										90										95										
ggt tcc tgc ggc ttg gag tac aac tta gat tac aca gag ctg ggc ctg	432																													
Gly Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu																														
100 105 110																														
aag aaa ctg aag gag tct gga aag cac cag ggc ttc tct gat tat tat	480																													
Lys Lys Leu Lys Glu Ser Gly Lys His Gln Gly Phe Ser Asp Tyr Tyr																														
115 120 125																														
cac aag ctg tgc tcc tca gat tcc tgt ggc ttt att acc att gca gta	528																													
His Lys Leu Cys Ser Ser Asp Ser Cys Gly Phe Ile Thr Ile Ala Val																														
130 135 140 145																														
ctg ttt gtt ctc gcc ttt gcg gtt tac aag ctg ttc ctc agc gat ggc	576																													
Leu Phe Val Leu Ala Phe Ala Val Tyr Lys Leu Phe Leu Ser Asp Gly																														
150 155 160																														
cag ggg tcg cct ccg ccg tat tct gag cac ccg cca tac tca gag cac	624																													
Gln Gly Ser Pro Pro Pro Tyr Ser Glu His Pro Pro Tyr Ser Glu His																														
165 170 175																														
tct cag agg ttt gcc agt gcc gca ggg gcg cct cct ccg ggc ttt aag	672																													
Ser Gln Arg Phe Ala Ser Ala Ala Gly Ala Pro Pro Gly Phe Lys																														
180 185 190																														
tcg gag ttc aca gga cca cag aat act ggc tat ggt gca agc tct ggc	720																													
Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly Tyr Gly Ala Ser Ser Gly																														
195 200 205																														
ttc ggg agt gct ttt gga ggc caa ggc tat ggc agt tca ggg ccg ggg	768																													
Phe Gly Ser Ala Phe Gly Gly Gln Gly Tyr Gly Ser Ser Gly Pro Gly																														
210 215 220 225																														
ttc tgg tct ggc ctg gga gct gga gga ctg ctt ggg tat ttg ttt ggc	816																													
Phe Trp Ser Gly Leu Gly Ala Gly Gly Leu Leu Gly Tyr Leu Phe Gly																														
230 235 240																														
agc aac aga gcg gcg acg cct ttc tca gac tcg tgg tac cat cca gcc	864																													
Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr His Pro Ala																														
245 250 255																														
tac cct cct tcc cac tct ggg gcc tgg aac agt cgg gcc tac tca ccc	912																													
Tyr Pro Pro Ser His Ser Gly Ala Trp Asn Ser Arg Ala Tyr Ser Pro																														
260 265 270																														
ctg ggt gga ggc gca ggg agc tat tgt gca tcc tct aat gca gac tcg	960																													
Leu Gly Gly Gly Ala Gly Ser Tyr Cys Ala Ser Ser Asn Ala Asp Ser																														
275 280 285																														
aga acc aga aca gca tca gga tat ggt ggc acc aga aga cgg taa	1005																													
Arg Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg																														
290 295 300																														

<210> 8
 <211> 334

<212> PRT
 <213> Mus musculus

<400> 8

Met Ala Val Ala Ala Val Gly Arg Pro Arg Ala Leu Arg Cys Pro Leu
 -30 -25 -20

Leu Leu Leu Leu Ser Leu Leu Leu Val Ala Gly Pro Ala Leu Gly Trp
 -15 -10 -5 -1 1

Asn Asp Pro Asp Arg Ile Leu Leu Arg Asp Val Lys Ala Leu Thr Leu
 5 10 15

Tyr Ser Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln
 20 25 30

Leu Lys Cys Val Gly Gly Thr Ala Gly Cys Glu Ala Tyr Thr Pro Arg
 35 40 45

Val Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp
 50 55 60 65

Glu Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val
 70 75 80

Val Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg
 85 90 95

Gly Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu
 100 105 110

Lys Lys Leu Lys Glu Ser Gly Lys His Gln Gly Phe Ser Asp Tyr Tyr
 115 120 125

His Lys Leu Cys Ser Ser Asp Ser Cys Gly Phe Ile Thr Ile Ala Val
 130 135 140 145

Leu Phe Val Leu Ala Phe Ala Val Tyr Lys Leu Phe Leu Ser Asp Gly
 150 155 160

Gln Gly Ser Pro Pro Pro Tyr Ser Glu His Pro Pro Tyr Ser Glu His
 165 170 175

Ser Gln Arg Phe Ala Ser Ala Ala Gly Ala Pro Pro Pro Gly Phe Lys
 180 185 190

Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly Tyr Gly Ala Ser Ser Gly
 195 200 205

Phe Gly Ser Ala Phe Gly Gly Gln Gly Tyr Gly Ser Ser Gly Pro Gly
 210 215 220 225

Phe Trp Ser Gly Leu Gly Ala Gly Gly Leu Leu Gly Tyr Leu Phe Gly
 230 235 240

Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr His Pro Ala
 245 250 255

Tyr Pro Pro Ser His Ser Gly Ala Trp Asn Ser Arg Ala Tyr Ser Pro
 260 265 270

Leu Gly Gly Gly Ala Gly Ser Tyr Cys Ala Ser Ser Asn Ala Asp Ser
 275 280 285

Arg Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
 290 295 300

<210> 9
 <211> 1053
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(1050)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(66)
 <223>

<220>
 <221> mat_peptide
 <222> (67)..()
 <223>

<400> 9
 atg cac ctg ctg ctt gca gcc gcg ttc ggg ctg ctg ctg ctg ctg ccg
 Met His Leu Leu Leu Ala Ala Ala Phe Gly Leu Leu Leu Leu Pro
 -20 -15 -10

48

ccg ccc ggg gcc gta gcc tcc cgg aag ccg acg atg tgc cag aga tgc	96
Pro Pro Gly Ala Val Ala Ser Arg Lys Pro Thr Met Cys Gln Arg Cys	
-5 -1 1 5 10	
cgg acg ctg gtg gac aag ttc aac cag ggg atg gcc aac acg gcc agg	144
Arg Thr Leu Val Asp Lys Phe Asn Gln Gly Met Ala Asn Thr Ala Arg	
15 20 25	
aag aat ttc ggt ggc ggc aac acg gcg tgg gaa gag aag acg ctg tct	192
Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr Leu Ser	
30 35 40	
aag tac gaa ttc agt gag atc cgg ctt ctg gag atc atg gag ggt ctg	240
Lys Tyr Glu Phe Ser Glu Ile Arg Leu Leu Glu Ile Met Glu Gly Leu	
45 50 55	
tgt gac agc agt gac ttt gag tgc aac caa ctc ttg gag cag cag gag	288
Cys Asp Ser Ser Asp Phe Glu Cys Asn Gln Leu Leu Glu Gln Gln Glu	
60 65 70	
gag cag cta gag gct tgg tgg cag aca ctg aag aag gag cac ccc aac	336
Glu Gln Leu Glu Ala Trp Trp Gln Thr Leu Lys Lys Glu His Pro Asn	
75 80 85 90	
cta ttt gag tgg ttc tgt gta cac aca ctg aaa gcg tgc tgt ctt cca	384
Leu Phe Glu Trp Phe Cys Val His Thr Leu Lys Ala Cys Cys Leu Pro	
95 100 105	
ggc acc tac ggg cca gac tgt caa aag tgc cag ggt ggg tcc gag agg	432
Gly Thr Tyr Gly Pro Asp Cys Gln Lys Cys Gln Gly Gly Ser Glu Arg	
110 115 120	
cct tgc agc gga aac ggc tat tgc agc gga gac ggc agc aga cag ggc	480
Pro Cys Ser Gly Asn Gly Tyr Cys Ser Gly Asp Gly Ser Arg Gln Gly	
125 130 135	
gac ggg tcc tgc cag tgt cac aca ggc tac aag gga cca ctg tgt att	528
Asp Gly Ser Cys Gln Cys His Thr Gly Tyr Lys Gly Pro Leu Cys Ile	
140 145 150	
gac tgc aca gac ggc ttc ttc agc ttg cag agg aac gag acc cac agc	576
Asp Cys Thr Asp Gly Phe Phe Ser Leu Gln Arg Asn Glu Thr His Ser	
155 160 165 170	
atc tgc tca gcc tgt gat gag tct tgc aag acc tgc tct ggt cca agc	624
Ile Cys Ser Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly Pro Ser	
175 180 185	
aac aaa gac tgt atc cag tgt gaa gtg ggc tgg gca cgt gtg gag gat	672
Asn Lys Asp Cys Ile Gln Cys Glu Val Gly Trp Ala Arg Val Glu Asp	
190 195 200	
gcc tgt gtg gat gtg gat gag tgt gca gca gag aca tct ccg tgc agc	720
Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Thr Ser Pro Cys Ser	
205 210 215	
gat ggc cag tac tgt gag aat gtc aac ggc tcg tac aca tgt gaa gac	768

Asp	Gly	Gln	Tyr	Cys	Glu	Asn	Val	Asn	Gly	Ser	Tyr	Thr	Cys	Glu	Asp	
220						225					230					
tgt	gat	tct	acc	tgc	gtg	ggc	tgt	aca	gga	aaa	ggc	cca	gcc	aac	tgt	816
Cys	Asp	Ser	Thr	Cys	Val	Gly	Cys	Thr	Gly	Lys	Gly	Pro	Ala	Asn	Cys	
235					240					245					250	
aag	gag	tgt	att	gcc	ggc	tac	acc	aag	gag	agt	gga	cag	tgc	aca	gat	864
Lys	Glu	Cys	Ile	Ala	Gly	Tyr	Thr	Lys	Glu	Ser	Gly	Gln	Cys	Thr	Asp	
				255					260					265		
ata	gat	gaa	tgc	tca	cta	gaa	gaa	aaa	gcc	tgt	aag	agg	aaa	aac	gaa	912
Ile	Asp	Glu	Cys	Ser	Leu	Glu	Glu	Lys	Ala	Cys	Lys	Arg	Lys	Asn	Glu	
			270					275					280			
aac	tgc	tac	aat	gtt	ccg	ggg	agc	ttc	gtg	tgc	gtg	tgt	ccg	gaa	ggc	960
Asn	Cys	Tyr	Asn	Val	Pro	Gly	Ser	Phe	Val	Cys	Val	Cys	Pro	Glu	Gly	
		285					290					295				
ttt	gag	gag	aca	gaa	gac	gct	tgt	gtg	cag	aca	gca	gaa	ggc	aaa	gtc	1008
Phe	Glu	Glu	Thr	Glu	Asp	Ala	Cys	Val	Gln	Thr	Ala	Glu	Gly	Lys	Val	
	300					305					310					
aca	gag	gaa	aac	ccc	aca	cag	cca	ccc	tcc	cgt	gag	gat	ttg	tga		1053
Thr	Glu	Glu	Asn	Pro	Thr	Gln	Pro	Pro	Ser	Arg	Glu	Asp	Leu			
315					320					325						

<210> 10
 <211> 350
 <212> PRT
 <213> Mus musculus

<400> 10

Met	His	Leu	Leu	Leu	Ala	Ala	Ala	Phe	Gly	Leu	Leu	Leu	Leu	Leu	Pro	
		-20					-15					-10				

Pro	Pro	Gly	Ala	Val	Ala	Ser	Arg	Lys	Pro	Thr	Met	Cys	Gln	Arg	Cys	
-5				-1	1				5						10	

Arg	Thr	Leu	Val	Asp	Lys	Phe	Asn	Gln	Gly	Met	Ala	Asn	Thr	Ala	Arg	
				15					20					25		

Lys	Asn	Phe	Gly	Gly	Gly	Asn	Thr	Ala	Trp	Glu	Glu	Lys	Thr	Leu	Ser	
			30					35					40			

Lys	Tyr	Glu	Phe	Ser	Glu	Ile	Arg	Leu	Leu	Glu	Ile	Met	Glu	Gly	Leu	
		45					50					55				

Cys	Asp	Ser	Ser	Asp	Phe	Glu	Cys	Asn	Gln	Leu	Leu	Glu	Gln	Gln	Glu	
	60					65					70					

Glu Gln Leu Glu Ala Trp Trp Gln Thr Leu Lys Lys Glu His Pro Asn
 75 80 85 90

Leu Phe Glu Trp Phe Cys Val His Thr Leu Lys Ala Cys Cys Leu Pro
 95 100 105

Gly Thr Tyr Gly Pro Asp Cys Gln Lys Cys Gln Gly Gly Ser Glu Arg
 110 115 120

Pro Cys Ser Gly Asn Gly Tyr Cys Ser Gly Asp Gly Ser Arg Gln Gly
 125 130 135

Asp Gly Ser Cys Gln Cys His Thr Gly Tyr Lys Gly Pro Leu Cys Ile
 140 145 150

Asp Cys Thr Asp Gly Phe Phe Ser Leu Gln Arg Asn Glu Thr His Ser
 155 160 165 170

Ile Cys Ser Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly Pro Ser
 175 180 185

Asn Lys Asp Cys Ile Gln Cys Glu Val Gly Trp Ala Arg Val Glu Asp
 190 195 200

Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Thr Ser Pro Cys Ser
 205 210 215

Asp Gly Gln Tyr Cys Glu Asn Val Asn Gly Ser Tyr Thr Cys Glu Asp
 220 225 230

Cys Asp Ser Thr Cys Val Gly Cys Thr Gly Lys Gly Pro Ala Asn Cys
 235 240 245 250

Lys Glu Cys Ile Ala Gly Tyr Thr Lys Glu Ser Gly Gln Cys Thr Asp
 255 260 265

Ile Asp Glu Cys Ser Leu Glu Glu Lys Ala Cys Lys Arg Lys Asn Glu
 270 275 280

Asn Cys Tyr Asn Val Pro Gly Ser Phe Val Cys Val Cys Pro Glu Gly
 285 290 295

Phe Glu Glu Thr Glu Asp Ala Cys Val Gln Thr Ala Glu Gly Lys Val
 300 305 310

Thr Glu Glu Asn Pro Thr Gln Pro Pro Ser Arg Glu Asp Leu
 315 320 325

<210> 11
 <211> 1254
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(1251)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(99)
 <223>

<220>
 <221> mat_peptide
 <222> (100)..()
 <223>

<400> 11
 atg ccc ccg cgc cca gga cgc ctc ctc cag ccg ctg gcc ggg ctg ccg 48
 Met Pro Pro Arg Pro Gly Arg Leu Leu Gln Pro Leu Ala Gly Leu Pro
 -30 -25 -20

gcc ctg gcc acg ctc ctg ctg ctg ctc ggg gcg cgc aaa ggc gcc cgg 96
 Ala Leu Ala Thr Leu Leu Leu Leu Leu Gly Ala Arg Lys Gly Ala Arg
 -15 -10 -5

gcc cag gag gtg gaa gcg gac agc ggg gtc gag cag gac ccg cac gcc 144
 Ala Gln Glu Val Glu Ala Asp Ser Gly Val Glu Gln Asp Pro His Ala
 -1 1 5 10 15

aag cac ctg tat acg gcc gac atg ttc acg cac ggg atc cag agc gcc 192
 Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile Gln Ser Ala
 20 25 30

gcg cac ttc gtc atg ttc ttc gcg ccc tgg tgt gga cac tgc cag cgg 240
 Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly His Cys Gln Arg
 35 40 45

ctg cag cca act tgg aat gac ctg gga gac aag tac aac agc atg gag 288
 Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys Tyr Asn Ser Met Glu
 50 55 60

gat gcc aag gtc tac gtg gcc aaa gtg gac tgc acg gct gat tcc gac 336
 Asp Ala Lys Val Tyr Val Ala Lys Val Asp Cys Thr Ala Asp Ser Asp
 65 70 75

gtg tgc tct gcc cag gga gtg cga gga tac ccc acc ctg aag ttt ttt	384
Val Cys Ser Ala Gln Gly Val Arg Gly Tyr Pro Thr Leu Lys Phe Phe	
80 85 90 95	
aag cct gga caa gaa gca gtg aag tac cag ggt cct aga gac ttt gaa	432
Lys Pro Gly Gln Glu Ala Val Lys Tyr Gln Gly Pro Arg Asp Phe Glu	
100 105 110	
aca ctg gaa aac tgg atg ctg cag aca ctg aac gag gag cca gcc aca	480
Thr Leu Glu Asn Trp Met Leu Gln Thr Leu Asn Glu Glu Pro Ala Thr	
115 120 125	
ccg gag ccg gaa gcg gaa cca ccc aga gcc cct gag ctc aaa cag ggg	528
Pro Glu Pro Glu Ala Glu Pro Pro Arg Ala Pro Glu Leu Lys Gln Gly	
130 135 140	
ttg tat gag ctc tcg gcc aac aac ttt gag ctg cat gtt tct caa ggc	576
Leu Tyr Glu Leu Ser Ala Asn Asn Phe Glu Leu His Val Ser Gln Gly	
145 150 155	
aac cac ttt atc aag ttc ttc gct ccg tgg tgc ggt cac tgc aaa gct	624
Asn His Phe Ile Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala	
160 165 170 175	
ctg gct cca acc tgg gag cag ctg gct ctg ggc ctt gaa cat tct gaa	672
Leu Ala Pro Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu	
180 185 190	
acc gtc aag att ggc aag gtt gac tgc acg cag cac tac gct gtc tgc	720
Thr Val Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Ala Val Cys	
195 200 205	
tca gag cat cag gtc aga ggc tat cca act ctg ctc tgg ttt cga gat	768
Ser Glu His Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp	
210 215 220	
ggc aag aag gtg gat cag tac aag gga aag cgg gac ttg gag tca ctg	816
Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser Leu	
225 230 235	
aga gac tat gtg cag tcc cag ctg cag ggt tca gag gca gct ccg gag	864
Arg Asp Tyr Val Gln Ser Gln Leu Gln Gly Ser Glu Ala Ala Pro Glu	
240 245 250 255	
act gtt gag ccg tca gag gcc cca gtg atg gct gct gag ccc acg ggt	912
Thr Val Glu Pro Ser Glu Ala Pro Val Met Ala Ala Glu Pro Thr Gly	
260 265 270	
gac aag ggc act gtg ctg gca ctc acc gag aag agc ttc gag gac act	960
Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Lys Ser Phe Glu Asp Thr	
275 280 285	
att gca cag ggg ata acc ttc gtc aag ttc tat gct ccg tgg tgt ggc	1008
Ile Ala Gln Gly Ile Thr Phe Val Lys Phe Tyr Ala Pro Trp Cys Gly	
290 295 300	

cac tgt aag aat ctg gct cct acc tgg gag gag ctc tct aaa aag gaa	1056
His Cys Lys Asn Leu Ala Pro Thr Trp Glu Glu Leu Ser Lys Lys Glu	
305 310 315	
ttc cca ggc ttg tca gat gtc acc atc gca gaa gtg gac tgc acc gct	1104
Phe Pro Gly Leu Ser Asp Val Thr Ile Ala Glu Val Asp Cys Thr Ala	
320 325 330 335	
gag cgc aat gtc tgc agc aag tac tcg gta cga ggt tat ccc acg ttg	1152
Glu Arg Asn Val Cys Ser Lys Tyr Ser Val Arg Gly Tyr Pro Thr Leu	
340 345 350	
ccg ctt ttc cga gga ggt gaa aaa gtg gga gac cac aac gga ggt aga	1200
Pro Leu Phe Arg Gly Gly Glu Lys Val Gly Asp His Asn Gly Gly Arg	
355 360 365	
gac ctc gac tcc tta cac agc ttt gtt ctg cgc cag gca aag gat gaa	1248
Asp Leu Asp Ser Leu His Ser Phe Val Leu Arg Gln Ala Lys Asp Glu	
370 375 380	
cta tag	1254
Leu	
<210> 12	
<211> 417	
<212> PRT	
<213> Mus musculus	
<400> 12	
Met Pro Pro Arg Pro Gly Arg Leu Leu Gln Pro Leu Ala Gly Leu Pro	
-30 -25 -20	
Ala Leu Ala Thr Leu Leu Leu Leu Leu Gly Ala Arg Lys Gly Ala Arg	
-15 -10 -5	
Ala Gln Glu Val Glu Ala Asp Ser Gly Val Glu Gln Asp Pro His Ala	
-1 1 5 10 15	
Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile Gln Ser Ala	
20 25 30	
Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly His Cys Gln Arg	
35 40 45	
Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys Tyr Asn Ser Met Glu	
50 55 60	
Asp Ala Lys Val Tyr Val Ala Lys Val Asp Cys Thr Ala Asp Ser Asp	

65

70

75

Val Cys Ser Ala Gln Gly Val Arg Gly Tyr Pro Thr Leu Lys Phe Phe
80 85 90 95

Lys Pro Gly Gln Glu Ala Val Lys Tyr Gln Gly Pro Arg Asp Phe Glu
100 105 110

Thr Leu Glu Asn Trp Met Leu Gln Thr Leu Asn Glu Glu Pro Ala Thr
115 120 125

Pro Glu Pro Glu Ala Glu Pro Pro Arg Ala Pro Glu Leu Lys Gln Gly
130 135 140

Leu Tyr Glu Leu Ser Ala Asn Asn Phe Glu Leu His Val Ser Gln Gly
145 150 155

Asn His Phe Ile Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala
160 165 170 175

Leu Ala Pro Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu
180 185 190

Thr Val Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Ala Val Cys
195 200 205

Ser Glu His Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp
210 215 220

Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser Leu
225 230 235

Arg Asp Tyr Val Gln Ser Gln Leu Gln Gly Ser Glu Ala Ala Pro Glu
240 245 250 255

Thr Val Glu Pro Ser Glu Ala Pro Val Met Ala Ala Glu Pro Thr Gly
260 265 270

Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Lys Ser Phe Glu Asp Thr
275 280 285

Ile Ala Gln Gly Ile Thr Phe Val Lys Phe Tyr Ala Pro Trp Cys Gly
290 295 300

His Cys Lys Asn Leu Ala Pro Thr Trp Glu Glu Leu Ser Lys Lys Glu
 305 310 315

Phe Pro Gly Leu Ser Asp Val Thr Ile Ala Glu Val Asp Cys Thr Ala
 320 325 330 335

Glu Arg Asn Val Cys Ser Lys Tyr Ser Val Arg Gly Tyr Pro Thr Leu
 340 345 350

Pro Leu Phe Arg Gly Gly Glu Lys Val Gly Asp His Asn Gly Gly Arg
 355 360 365

Asp Leu Asp Ser Leu His Ser Phe Val Leu Arg Gln Ala Lys Asp Glu
 370 375 380

Leu

<210> 13
 <211> 843
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(840)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(99)
 <223>

<220>
 <221> mat_peptide
 <222> (100)..()
 <223>

<400> 13
 atg ccc ccg cgc cca gga cgc ctc ctc cag ccg ctg gcc ggg ctg ccg 48
 Met Pro Pro Arg Pro Gly Arg Leu Leu Gln Pro Leu Ala Gly Leu Pro
 -30 -25 -20

gcc ctg gcc acg ctc ctg ctg ctg ctc ggg gcg cgc aaa ggc gcc cgg 96
 Ala Leu Ala Thr Leu Leu Leu Leu Leu Gly Ala Arg Lys Gly Ala Arg
 -15 -10 -5

gcc cag gag gtg gaa gcg gac agc ggg gtc gag cag gac ccg cac gcc 144
 Ala Gln Glu Val Glu Ala Asp Ser Gly Val Glu Gln Asp Pro His Ala

-1	1		5		10		15									
aag	cac	ctg	tat	acg	gcc	gac	atg	ttc	acg	cac	ggg	atc	cag	agc	gcc	192
Lys	His	Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile	Gln	Ser	Ala	
				20					25					30		
gcg	cac	ttc	gtc	atg	ttc	ttc	gcg	ccc	tgg	tgt	gga	cac	tgc	cag	cgg	240
Ala	His	Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Gln	Arg	
			35					40					45			
ctg	cag	cca	act	tgg	aat	gac	ctg	gga	gac	aag	tac	aac	agc	atg	gag	288
Leu	Gln	Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys	Tyr	Asn	Ser	Met	Glu	
		50					55					60				
gat	gcc	aag	gtc	tac	gtg	gcc	aaa	gtg	gac	tgc	acg	gct	gat	tcc	gac	336
Asp	Ala	Lys	Val	Tyr	Val	Ala	Lys	Val	Asp	Cys	Thr	Ala	Asp	Ser	Asp	
	65					70				75						
gtg	tgc	tct	gcc	cag	gga	gtg	cga	gga	tac	ccc	acc	ctg	aag	ttt	ttt	384
Val	Cys	Ser	Ala	Gln	Gly	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Lys	Phe	Phe	
80					85					90				95		
aag	cct	gga	caa	gaa	gca	gtg	aag	tac	cag	ggt	cct	aga	gac	ttt	gaa	432
Lys	Pro	Gly	Gln	Glu	Ala	Val	Lys	Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Glu	
			100						105					110		
aca	ctg	gaa	aac	tgg	atg	ctg	cag	aca	ctg	aac	gag	gag	cca	gcc	aca	480
Thr	Leu	Glu	Asn	Trp	Met	Leu	Gln	Thr	Leu	Asn	Glu	Glu	Pro	Ala	Thr	
			115					120					125			
ccg	gag	ccg	gaa	gcg	gaa	cca	ccc	aga	gcc	cct	gag	ctc	aaa	cag	ggg	528
Pro	Glu	Pro	Glu	Ala	Glu	Pro	Pro	Arg	Ala	Pro	Glu	Leu	Lys	Gln	Gly	
		130					135					140				
ttg	tat	gag	ctc	tcg	gcc	aac	aac	ttt	gag	ctg	cat	gtt	tct	caa	ggc	576
Leu	Tyr	Glu	Leu	Ser	Ala	Asn	Asn	Phe	Glu	Leu	His	Val	Ser	Gln	Gly	
	145					150					155					
aac	cac	ttt	atc	aag	ttc	ttc	gct	ccg	tgg	tgc	ggt	cac	tgc	aaa	gct	624
Asn	His	Phe	Ile	Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	
160					165				170					175		
ctg	gct	cca	acc	tgg	gag	cag	ctg	gct	ctg	ggc	ctt	gaa	cat	tct	gaa	672
Leu	Ala	Pro	Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	
				180					185					190		
acc	gtc	aag	att	ggc	aag	gtt	gac	tgc	acg	cag	cac	tac	gct	gtc	tgc	720
Thr	Val	Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Ala	Val	Cys	
			195					200					205			
tca	gag	cat	cag	gtc	aga	ggc	tat	cca	act	ctg	ctc	tgg	ttt	cga	gat	768
Ser	Glu	His	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	
		210					215					220				
ggc	aag	aag	gtg	gat	cag	tac	aag	gga	aag	cgg	gac	ttg	gag	tca	ctg	816
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	Leu	
	225					230					235					

aga gac tat gtg cag tcc cag ctg tag
 Arg Asp Tyr Val Gln Ser Gln Leu
 240 245

843

<210> 14
 <211> 280
 <212> PRT
 <213> Mus musculus

<400> 14

Met Pro Pro Arg Pro Gly Arg Leu Leu Gln Pro Leu Ala Gly Leu Pro
 -30 -25 -20

Ala Leu Ala Thr Leu Leu Leu Leu Leu Gly Ala Arg Lys Gly Ala Arg
 -15 -10 -5

Ala Gln Glu Val Glu Ala Asp Ser Gly Val Glu Gln Asp Pro His Ala
 -1 1 5 10 15

Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile Gln Ser Ala
 20 25 30

Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly His Cys Gln Arg
 35 40 45

Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys Tyr Asn Ser Met Glu
 50 55 60

Asp Ala Lys Val Tyr Val Ala Lys Val Asp Cys Thr Ala Asp Ser Asp
 65 70 75

Val Cys Ser Ala Gln Gly Val Arg Gly Tyr Pro Thr Leu Lys Phe Phe
 80 85 90 95

Lys Pro Gly Gln Glu Ala Val Lys Tyr Gln Gly Pro Arg Asp Phe Glu
 100 105 110

Thr Leu Glu Asn Trp Met Leu Gln Thr Leu Asn Glu Glu Pro Ala Thr
 115 120 125

Pro Glu Pro Glu Ala Glu Pro Pro Arg Ala Pro Glu Leu Lys Gln Gly
 130 135 140

Leu Tyr Glu Leu Ser Ala Asn Asn Phe Glu Leu His Val Ser Gln Gly
 145 150 155

Asn His Phe Ile Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala
 160 165 170 175

Leu Ala Pro Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu
 180 185 190

Thr Val Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Ala Val Cys
 195 200 205

Ser Glu His Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp
 210 215 220

Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser Leu
 225 230 235

Arg Asp Tyr Val Gln Ser Gln Leu
 240 245

<210> 15
 <211> 1269
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(1266)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(63)
 <223>

<220>
 <221> mat_peptide
 <222> (64)..()
 <223>

<400> 15
 atg cgt gcg ggc cgg tgt gcc gcg gcg ctg ctg ctg ctg cta ctg agc 48
 Met Arg Ala Gly Arg Cys Ala Ala Ala Leu Leu Leu Leu Leu Ser
 -20 -15 -10

ggc gcg ggg cgc gcg atc ggc tcc gag gac atc gtg gta ggc tgc ggg 96
 Gly Ala Gly Arg Ala Ile Gly Ser Glu Asp Ile Val Val Gly Cys Gly
 -5 -1 1 5 10

ggt ttc gtg aag tcg gac gtg gag atc aac tac tcg ctc atc gag ata	144
Gly Phe Val Lys Ser Asp Val Glu Ile Asn Tyr Ser Leu Ile Glu Ile	
15 20 25	
aag tta tac acc aag cat ggg act ttg aaa tat cag acg gac tgt gct	192
Lys Leu Tyr Thr Lys His Gly Thr Leu Lys Tyr Gln Thr Asp Cys Ala	
30 35 40	
cct aac aac ggc tac ttt atg atc ccc ttg tat gat aag ggg gat ttc	240
Pro Asn Asn Gly Tyr Phe Met Ile Pro Leu Tyr Asp Lys Gly Asp Phe	
45 50 55	
atc ctg aag atc gaa cct cct ctg ggc tgg agt ttt gag cca acc aac	288
Ile Leu Lys Ile Glu Pro Pro Leu Gly Trp Ser Phe Glu Pro Thr Asn	
60 65 70 75	
gtg gag ctg cga gtg gat ggt gtg agc gac atc tgc acg aag ggc ggg	336
Val Glu Leu Arg Val Asp Gly Val Ser Asp Ile Cys Thr Lys Gly Gly	
80 85 90	
gac atc aac ttc ctg ttc acc ggc ttc tct gtg aat ggc aag gtc ctc	384
Asp Ile Asn Phe Leu Phe Thr Gly Phe Ser Val Asn Gly Lys Val Leu	
95 100 105	
agc aaa ggg cag ccc ctg ggc cca gca gga gtt cag gta tcc ctg aga	432
Ser Lys Gly Gln Pro Leu Gly Pro Ala Gly Val Gln Val Ser Leu Arg	
110 115 120	
agc acc ggt gct gac tcg aag atc cag tct aca gtc acg cag cct ggc	480
Ser Thr Gly Ala Asp Ser Lys Ile Gln Ser Thr Val Thr Gln Pro Gly	
125 130 135	
gga aag ttt gcg ttt ttc aaa gtt ctt cct gga gat tat gaa atc ctt	528
Gly Lys Phe Ala Phe Phe Lys Val Leu Pro Gly Asp Tyr Glu Ile Leu	
140 145 150 155	
gca act cac ccg acc tgg gcg ctg aag gag gca agt acc acg gtg cgt	576
Ala Thr His Pro Thr Trp Ala Leu Lys Glu Ala Ser Thr Thr Val Arg	
160 165 170	
gtg acg aac tcg aat gct aac gca gct ggt ccc ctc ata gtg gct ggc	624
Val Thr Asn Ser Asn Ala Asn Ala Ala Gly Pro Leu Ile Val Ala Gly	
175 180 185	
tat aat gtg tcc ggc tct gtc cgc agt gac ggg gag ccc atg aaa ggg	672
Tyr Asn Val Ser Gly Ser Val Arg Ser Asp Gly Glu Pro Met Lys Gly	
190 195 200	
gtg aag ttt ctt ctc ttt tct tct tta gtg aac aaa gag gat gtc ctg	720
Val Lys Phe Leu Leu Phe Ser Ser Leu Val Asn Lys Glu Asp Val Leu	
205 210 215	
ggc tgc aat gtg tcc cca gtg tcc ggg ttc cag ccc cca gat gag agc	768
Gly Cys Asn Val Ser Pro Val Ser Gly Phe Gln Pro Pro Asp Glu Ser	
220 225 230 235	
ctg gtt tat ctg tgc tat gcg gtc tcc aaa gaa gac ggc cca ttt tct	816

Leu Val Tyr	Leu Cys Tyr	Ala Val Ser	Lys Glu Asp	Gly Pro Phe	Ser	
	240		245		250	
ttc tat tcc ttg ccg agt ggg ggc tac act gtg gtg ccc ttc tac cga						864
Phe Tyr Ser	Leu Pro Ser	Gly Gly Tyr	Thr Val Val	Pro Phe Tyr	Arg	
	255		260		265	
gga gaa agg atc acc ttc gac gtg gcg ccc tcc cgg ctt gac ttc acg						912
Gly Glu Arg	Ile Thr Phe	Asp Val Ala	Pro Ser Arg	Leu Asp Phe	Thr	
	270		275		280	
gtg gag cac ggc agc ctg aga atc gag cct gta ttc cac gtc atg ggc						960
Val Glu His	Gly Ser Leu	Arg Ile Glu	Pro Val Phe	His Val Met	Gly	
	285		290		295	
ttc tct gtc acc ggg aga gtc ttg aat gga cct gac gga gaa ggc gtc						1008
Phe Ser Val	Thr Gly Arg	Val Leu Asn	Gly Pro Asp	Gly Glu Gly	Val	
300		305		310	315	
ccg gag gct gtg gtc acc ctg aac aac cag att aaa gtc aaa acg aag						1056
Pro Glu Ala	Val Val Thr	Leu Asn Asn	Gln Ile Lys	Val Lys Thr	Lys	
	320		325		330	
gcc gac ggc tcc ttc cgc ctg gag aac ata acg aca ggg aca tac acc						1104
Ala Asp Gly	Ser Phe Arg	Leu Glu Asn	Ile Thr Thr	Gly Thr Tyr	Thr	
	335		340		345	
atc cac gct cag aag gag cac ctc tac ttc gag atg gtc acc atc aaa						1152
Ile His Ala	Gln Lys Glu	His Leu Tyr	Phe Glu Met	Val Thr Ile	Lys	
	350		355		360	
att gcc ccc aat acc cca cag ctg gct gac ctc atc gct aca ggg ctt						1200
Ile Ala Pro	Asn Thr Pro	Gln Leu Ala	Asp Leu Ile	Ala Thr Gly	Leu	
	365		370		375	
ctc cct gca ggt tca gca tct gtg gtc aga tcg cca tcg tcc gct ccc						1248
Leu Pro Ala	Gly Ser Ala	Ser Val Val	Arg Ser Pro	Ser Ser Ala	Pro	
380		385		390	395	
ccg aca cca tca agc aga tga						1269
Pro Thr Pro	Ser Ser Arg					
	400					

<210> 16
 <211> 422
 <212> PRT
 <213> Mus musculus

<400> 16

Met Arg Ala Gly Arg Cys Ala Ala Ala Leu Leu Leu Leu Leu Ser	
-20	-15 -10

Gly Ala Gly Arg Ala Ile Gly Ser Glu Asp Ile Val Val Gly Cys Gly	
-5	-1 1 5 10

Gly	Phe	Val	Lys	Ser	Asp	Val	Glu	Ile	Asn	Tyr	Ser	Leu	Ile	Glu	Ile	15	20	25	
Lys	Leu	Tyr	Thr	Lys	His	Gly	Thr	Leu	Lys	Tyr	Gln	Thr	Asp	Cys	Ala	30	35	40	
Pro	Asn	Asn	Gly	Tyr	Phe	Met	Ile	Pro	Leu	Tyr	Asp	Lys	Gly	Asp	Phe	45	50	55	
Ile	Leu	Lys	Ile	Glu	Pro	Pro	Leu	Gly	Trp	Ser	Phe	Glu	Pro	Thr	Asn	60	65	70	75
Val	Glu	Leu	Arg	Val	Asp	Gly	Val	Ser	Asp	Ile	Cys	Thr	Lys	Gly	Gly	80	85	90	
Asp	Ile	Asn	Phe	Leu	Phe	Thr	Gly	Phe	Ser	Val	Asn	Gly	Lys	Val	Leu	95	100	105	
Ser	Lys	Gly	Gln	Pro	Leu	Gly	Pro	Ala	Gly	Val	Gln	Val	Ser	Leu	Arg	110	115	120	
Ser	Thr	Gly	Ala	Asp	Ser	Lys	Ile	Gln	Ser	Thr	Val	Thr	Gln	Pro	Gly	125	130	135	
Gly	Lys	Phe	Ala	Phe	Phe	Lys	Val	Leu	Pro	Gly	Asp	Tyr	Glu	Ile	Leu	140	145	150	155
Ala	Thr	His	Pro	Thr	Trp	Ala	Leu	Lys	Glu	Ala	Ser	Thr	Thr	Val	Arg	160	165	170	
Val	Thr	Asn	Ser	Asn	Ala	Asn	Ala	Ala	Gly	Pro	Leu	Ile	Val	Ala	Gly	175	180	185	
Tyr	Asn	Val	Ser	Gly	Ser	Val	Arg	Ser	Asp	Gly	Glu	Pro	Met	Lys	Gly	190	195	200	
Val	Lys	Phe	Leu	Leu	Phe	Ser	Ser	Leu	Val	Asn	Lys	Glu	Asp	Val	Leu	205	210	215	
Gly	Cys	Asn	Val	Ser	Pro	Val	Ser	Gly	Phe	Gln	Pro	Pro	Asp	Glu	Ser	220	225	230	235

Leu Val Tyr Leu Cys Tyr Ala Val Ser Lys Glu Asp Gly Pro Phe Ser
240 245 250

Phe Tyr Ser Leu Pro Ser Gly Gly Tyr Thr Val Val Pro Phe Tyr Arg
255 260 265

Gly Glu Arg Ile Thr Phe Asp Val Ala Pro Ser Arg Leu Asp Phe Thr
270 275 280

Val Glu His Gly Ser Leu Arg Ile Glu Pro Val Phe His Val Met Gly
285 290 295

Phe Ser Val Thr Gly Arg Val Leu Asn Gly Pro Asp Gly Glu Gly Val
300 305 310 315

Pro Glu Ala Val Val Thr Leu Asn Asn Gln Ile Lys Val Lys Thr Lys
320 325 330

Ala Asp Gly Ser Phe Arg Leu Glu Asn Ile Thr Thr Gly Thr Tyr Thr
335 340 345

Ile His Ala Gln Lys Glu His Leu Tyr Phe Glu Met Val Thr Ile Lys
350 355 360

Ile Ala Pro Asn Thr Pro Gln Leu Ala Asp Leu Ile Ala Thr Gly Leu
365 370 375

Leu Pro Ala Gly Ser Ala Ser Val Val Arg Ser Pro Ser Ser Ala Pro
380 385 390 395

Pro Thr Pro Ser Ser Arg
400

<210> 17
<211> 531
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(528)
<223>

<220>
<221> sig_peptide

```

<222> (1)..(81)
<223>

<220>
<221> mat_peptide
<222> (82)..()
<223>

<400> 17
atg gca gcg agc acg gac ata gct ggg ctg gag gag agc ttc cgg aag      48
Met Ala Ala Ser Thr Asp Ile Ala Gly Leu Glu Glu Ser Phe Arg Lys
      -25                -20                -15

ttt gcc atc cat ggc gac ccc aag gcc agc ggg caa gag atg aat ggc      96
Phe Ala Ile His Gly Asp Pro Lys Ala Ser Gly Gln Glu Met Asn Gly
      -10                -5                -1 1                5

aag aac tgg gcc aag ctg tgc aag gac tgt aag gtg gcc gac gga aag      144
Lys Asn Trp Ala Lys Leu Cys Lys Asp Cys Lys Val Ala Asp Gly Lys
              10                15                20

gcc gta acg ggc acc gac gtc gac atc gtc ttc tcc aaa gtc aag gcg      192
Ala Val Thr Gly Thr Asp Val Asp Ile Val Phe Ser Lys Val Lys Ala
              25                30                35

aaa tct gct aga gta atc aac tat gag gag ttc aag aag gcc ctg gaa      240
Lys Ser Ala Arg Val Ile Asn Tyr Glu Glu Phe Lys Lys Ala Leu Glu
              40                45                50

gag ctg gca act aag cgg ttc aag ggg aag tcc aag gag gag gcc ttt      288
Glu Leu Ala Thr Lys Arg Phe Lys Gly Lys Ser Lys Glu Glu Ala Phe
              55                60                65

gat gcc atc tgc cag ctg ata gcg ggc aag gaa ccg gcc aac att ggc      336
Asp Ala Ile Cys Gln Leu Ile Ala Gly Lys Glu Pro Ala Asn Ile Gly
              70                75                80                85

gtc acc aaa gct aaa acg ggt ggt gct gtg gac cgg ctg acg gac acc      384
Val Thr Lys Ala Lys Thr Gly Gly Ala Val Asp Arg Leu Thr Asp Thr
              90                95                100

agt aag tat acg ggc tcc cac aaa gaa cgc ttt gat gag agc ggc aag      432
Ser Lys Tyr Thr Gly Ser His Lys Glu Arg Phe Asp Glu Ser Gly Lys
              105                110                115

gga aag ggc atc gct gga cgg cag gac atc ctg gac gac agt ggc tac      480
Gly Lys Gly Ile Ala Gly Arg Gln Asp Ile Leu Asp Asp Ser Gly Tyr
              120                125                130

gtg agt gcc tac aaa aac gca ggc acc tat gac gcc aag gtg aag aag      528
Val Ser Ala Tyr Lys Asn Ala Gly Thr Tyr Asp Ala Lys Val Lys Lys
              135                140                145

tga                                                                    531

<210> 18

```

<211> 176
 <212> PRT
 <213> Mus musculus

<400> 18

Met Ala Ala Ser Thr Asp Ile Ala Gly Leu Glu Glu Ser Phe Arg Lys
 -25 -20 -15

Phe Ala Ile His Gly Asp Pro Lys Ala Ser Gly Gln Glu Met Asn Gly
 -10 -5 -1 1 5

Lys Asn Trp Ala Lys Leu Cys Lys Asp Cys Lys Val Ala Asp Gly Lys
 10 15 20

Ala Val Thr Gly Thr Asp Val Asp Ile Val Phe Ser Lys Val Lys Ala
 25 30 35

Lys Ser Ala Arg Val Ile Asn Tyr Glu Glu Phe Lys Lys Ala Leu Glu
 40 45 50

Glu Leu Ala Thr Lys Arg Phe Lys Gly Lys Ser Lys Glu Glu Ala Phe
 55 60 65

Asp Ala Ile Cys Gln Leu Ile Ala Gly Lys Glu Pro Ala Asn Ile Gly
 70 75 80 85

Val Thr Lys Ala Lys Thr Gly Gly Ala Val Asp Arg Leu Thr Asp Thr
 90 95 100

Ser Lys Tyr Thr Gly Ser His Lys Glu Arg Phe Asp Glu Ser Gly Lys
 105 110 115

Gly Lys Gly Ile Ala Gly Arg Gln Asp Ile Leu Asp Asp Ser Gly Tyr
 120 125 130

Val Ser Ala Tyr Lys Asn Ala Gly Thr Tyr Asp Ala Lys Val Lys Lys
 135 140 145

<210> 19
 <211> 588
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS

<222> (1)..(585)

<223>

<220>

<221> sig_peptide

<222> (1)..(51)

<223>

<220>

<221> mat_peptide

<222> (52)..()

<223>

<400> 19

atg gct tca gga tgg ttt tac ctg tcc tgc atg gtg ctg gga tcg ctg	48
Met Ala Ser Gly Trp Phe Tyr Leu Ser Cys Met Val Leu Gly Ser Leu	
-15 -10 -5	

gga tcg atg tgc atc ctc ttc act gcc tac tgg atg cag tac tgg cgc	96
Gly Ser Met Cys Ile Leu Phe Thr Ala Tyr Trp Met Gln Tyr Trp Arg	
-1 1 5 10 15	

ggg ggc ttt gcc tgg gat ggc acg gtg ctc atg ttt aac tgg cac cca	144
Gly Gly Phe Ala Trp Asp Gly Thr Val Leu Met Phe Asn Trp His Pro	
20 25 30	

gtg ctc atg gtt gcc ggc atg gtg gtg ctc tat gga gct gcc tca ctg	192
Val Leu Met Val Ala Gly Met Val Val Leu Tyr Gly Ala Ala Ser Leu	
35 40 45	

gtg tac cgc ctg cct tca tcg tgg gtg ggg ccc agg ctg ccc tgg aaa	240
Val Tyr Arg Leu Pro Ser Ser Trp Val Gly Pro Arg Leu Pro Trp Lys	
50 55 60	

gtt ctc cat gca gca ctg cac ctg ctg gcc ttc acc tgc act gtg gtg	288
Val Leu His Ala Ala Leu His Leu Leu Ala Phe Thr Cys Thr Val Val	
65 70 75	

ggg ctg att gcc gtc ttt cgg ttt cac aac cac tcg aga atc gca cac	336
Gly Leu Ile Ala Val Phe Arg Phe His Asn His Ser Arg Ile Ala His	
80 85 90 95	

ctc tac tcc ctg cac agc tgg ctg ggt atc acc act gta gtc ctc ttc	384
Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Val Leu Phe	
100 105 110	

gcc tgc cag tgg ttc ctg ggc ttt gct gtc ttc ctc ctg ccc tgg gca	432
Ala Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala	
115 120 125	

tcc cag tgg ctg cga agc ctc ctg aaa cct ctg cat gta ttc ttt gga	480
Ser Gln Trp Leu Arg Ser Leu Leu Lys Pro Leu His Val Phe Phe Gly	
130 135 140	

gcc tgc atc ctt tcc ctg tcc atc aca tct gtt att tcc ggc atc aat	528
Ala Cys Ile Leu Ser Leu Ser Ile Thr Ser Val Ile Ser Gly Ile Asn	
145 150 155	

gag aag ctt ttc ttt gtt ttg aaa aat gcc acc aag ccc cta ctc cag 576
Glu Lys Leu Phe Phe Val Leu Lys Asn Ala Thr Lys Pro Leu Leu Gln
160 165 170 175

```
<210> 20
<211> 195
<212> PRT
<213> Mus musculus
```

Met Ala Ser Gly Trp Phe Tyr Leu Ser Cys Met Val Leu Gly Ser Leu
-15 -10 -5

Gly Gly Phe Ala Trp Asp Gly Thr Val Leu Met Phe Asn Trp His Pro
20 25 30

Val Tyr Arg Leu Pro Ser Ser Trp Val Gly Pro Arg Leu Pro Trp Lys
50 55 60

Gly Leu Ile Ala Val Phe Arg Phe His Asn His Ser Arg Ile Ala His
80 85 90 95

Ala Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
115 120 125

Ala Cys Ile Leu Ser Leu Ser Ile Thr Ser Val Ile Ser Gly Ile Asn
 145 150 155

Glu Lys Leu Phe Phe Val Leu Lys Asn Ala Thr Lys Pro Leu Leu Gln
 160 165 170 175

Pro Ala Trp

<210> 21
 <211> 3147
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(3144)
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(147)
 <223>

<220>
 <221> mat_peptide
 <222> (148)..()
 <223>

<400> 21
 atg gag aag aga ctg gga gtc aag cca agt ccc gct tcc tgg gtt ttg 48
 Met Glu Lys Arg Leu Gly Val Lys Pro Ser Pro Ala Ser Trp Val Leu
 -45 -40 -35
 cca gga tat tgt tgg cag aca tca gtg aag ctg ccg aga agc ctg tac 96
 Pro Gly Tyr Cys Trp Gln Thr Ser Val Lys Leu Pro Arg Ser Leu Tyr
 -30 -25 -20
 ctg ctt tac agt ttc ttc tgc ttc agc gtt ctg tgg ttg tca aca gat 144
 Leu Leu Tyr Ser Phe Phe Cys Phe Ser Val Leu Trp Leu Ser Thr Asp
 -15 -10 -5
 gct gat gag agc aga tgc caa cag ggg aag aca ctt tat gga gct ggc 192
 Ala Asp Glu Ser Arg Cys Gln Gln Gly Lys Thr Leu Tyr Gly Ala Gly
 -1 1 5 10 15
 ttg aga act gag gga gaa aat cac ctc cgg ctt ctt gca gga agc ctg 240
 Leu Arg Thr Glu Gly Glu Asn His Leu Arg Leu Leu Ala Gly Ser Leu
 20 25 30
 cct ttc cac gcc tgt cgg gct gcc tgc tgc cgg gac tct gcc tgc cac 288
 Pro Phe His Ala Cys Arg Ala Ala Cys Cys Arg Asp Ser Ala Cys His
 35 40 45

gct cta tgg tgg ctg gaa ggg atg tgc ttt cag gct gac tgc agc aag Ala Leu Trp Trp Leu Glu Gly Met Cys Phe Gln Ala Asp Cys Ser Lys 50 55 60	336
ccc cag agc tgc cag cct ttt agg aca gac tct tcc aat tcc atg ctg Pro Gln Ser Cys Gln Pro Phe Arg Thr Asp Ser Ser Asn Ser Met Leu 65 70 75	384
atc att ttt caa aaa tcc caa act aca gat gat ttg ggc ctt ctg cct Ile Ile Phe Gln Lys Ser Gln Thr Thr Asp Asp Leu Gly Leu Leu Pro 80 85 90 95	432
gaa gat gat gaa cca cat ctt ctg agg cta ggc tgg ggc agg aca tcg Glu Asp Asp Glu Pro His Leu Leu Arg Leu Gly Trp Gly Arg Thr Ser 100 105 110	480
tgg agg agg cag agc ctt ctt ggg gct ccc ctc acc ctt tct gta ccc Trp Arg Arg Gln Ser Leu Leu Gly Ala Pro Leu Thr Leu Ser Val Pro 115 120 125	528
tct agt cac cac cag agc tta ctc agg gat cgg cag aag aga gat ctc Ser Ser His His Gln Ser Leu Leu Arg Asp Arg Gln Lys Arg Asp Leu 130 135 140	576
agt gtg gta cct aca cat gga gcg atg cag cat tct aaa gtg aat cac Ser Val Val Pro Thr His Gly Ala Met Gln His Ser Lys Val Asn His 145 150 155	624
tcc gag gaa gca ggt gct ctg agt ccc acc tct gca gag gtc cgc aaa Ser Glu Glu Ala Gly Ala Leu Ser Pro Thr Ser Ala Glu Val Arg Lys 160 165 170 175	672
acc att aca gtt gcc ggt tcc ttc acc agt aac cac act aca cag act Thr Ile Thr Val Ala Gly Ser Phe Thr Ser Asn His Thr Thr Gln Thr 180 185 190	720
cct gag tgg ccc aag aat gtg tcc atc cat cct gaa cca tcc gag cac Pro Glu Trp Pro Lys Asn Val Ser Ile His Pro Glu Pro Ser Glu His 195 200 205	768
tcc agt cct gta tct ggt act ccg caa gta aaa agc act gag cac agt Ser Ser Pro Val Ser Gly Thr Pro Gln Val Lys Ser Thr Glu His Ser 210 215 220	816
cca act gat gcc cct ctg cca gtg gcc ccc tcc tac agc tat gcc acc Pro Thr Asp Ala Pro Leu Pro Val Ala Pro Ser Tyr Ser Tyr Ala Thr 225 230 235	864
ccc acg ccc cag gcc tct tct cag agc acc tca gca cca cac cca gtt Pro Thr Pro Gln Ala Ser Ser Gln Ser Thr Ser Ala Pro His Pro Val 240 245 250 255	912
gta aag gag ctg gtg gtg tct gct ggg aag agc gtc cag atc acc ctg Val Lys Glu Leu Val Val Ser Ala Gly Lys Ser Val Gln Ile Thr Leu 260 265 270	960
cct aag aat gaa gtt cag tta aat gcc ttc gtc ctt cca gaa gca gag	1008

Pro Lys Asn Glu Val Gln Leu Asn Ala Phe Val Leu Pro Glu Ala Glu	
275 280 285	
cca gga gaa acc tac acc tac gac tgg cag ctg atc act cat cct aca	1056
Pro Gly Glu Thr Tyr Thr Tyr Asp Trp Gln Leu Ile Thr His Pro Thr	
290 295 300	
gac tac agt gga gag gtg gag agg aaa cat tcc cag agc ctc caa ctg	1104
Asp Tyr Ser Gly Glu Val Glu Arg Lys His Ser Gln Ser Leu Gln Leu	
305 310 315	
tcc aag ctg act cca ggc ctg tac gaa ttc aag gtg act gtg gat ggc	1152
Ser Lys Leu Thr Pro Gly Leu Tyr Glu Phe Lys Val Thr Val Asp Gly	
320 325 330 335	
cag aat gcc cat ggg gaa ggc tac gtg aat gtg aca gtg aaa cca gag	1200
Gln Asn Ala His Gly Glu Gly Tyr Val Asn Val Thr Val Lys Pro Glu	
340 345 350	
ccc cgt aag aac cgg cct ccc gtt gct gtg gtg tca cct cag ttc cag	1248
Pro Arg Lys Asn Arg Pro Pro Val Ala Val Val Ser Pro Gln Phe Gln	
355 360 365	
gag atc tcg ctg cca acc act tct acc atc att gat ggc agc cag agc	1296
Glu Ile Ser Leu Pro Thr Thr Ser Thr Ile Ile Asp Gly Ser Gln Ser	
370 375 380	
acg gat gac gat aaa att gtc cag tac cac tgg gaa gag ctt aag ggg	1344
Thr Asp Asp Asp Lys Ile Val Gln Tyr His Trp Glu Glu Leu Lys Gly	
385 390 395	
ccc ctg aga gaa gag aag atc tct gaa gac aca gcc ata cta aaa ctt	1392
Pro Leu Arg Glu Glu Lys Ile Ser Glu Asp Thr Ala Ile Leu Lys Leu	
400 405 410 415	
agt aag ctc gtc ccg ggg aac tac acc ttc agc tta act gtt gtc gac	1440
Ser Lys Leu Val Pro Gly Asn Tyr Thr Phe Ser Leu Thr Val Val Asp	
420 425 430	
tct gac ggg gct acc aac tcc acc act gca agc ctg act gtg aac aaa	1488
Ser Asp Gly Ala Thr Asn Ser Thr Thr Ala Ser Leu Thr Val Asn Lys	
435 440 445	
gct gtg gac tac cct ccc gtg gcc aat gca ggc ccc aac caa gtg atc	1536
Ala Val Asp Tyr Pro Pro Val Ala Asn Ala Gly Pro Asn Gln Val Ile	
450 455 460	
acc ctg cct cag aac tcc atc acc ctc ttt gga aac cag agc acg gat	1584
Thr Leu Pro Gln Asn Ser Ile Thr Leu Phe Gly Asn Gln Ser Thr Asp	
465 470 475	
gac cac ggc atc acc agc tat gag tgg tcg ctc agc ccg agc agc aaa	1632
Asp His Gly Ile Thr Ser Tyr Glu Trp Ser Leu Ser Pro Ser Ser Lys	
480 485 490 495	
ggg aag gtg gtg gag atg cag gga gtt aga acg cca gcc ctg cag ctg	1680
Gly Lys Val Val Glu Met Gln Gly Val Arg Thr Pro Ala Leu Gln Leu	

500	505	510	
tcc gca atg caa gaa gga gac tat acc tac cag ctc aca gtg act gac Ser Ala Met Gln Glu Gly Asp Tyr Thr Tyr Gln Leu Thr Val Thr Asp 515 520 525			1728
acc gca gga caa cag gcc acc gcc caa gtg act gtg att gtg cag cct Thr Ala Gly Gln Gln Ala Thr Ala Gln Val Thr Val Ile Val Gln Pro 530 535 540			1776
gag aac aac aag cct cct cag gca gat gca ggc cca gac aaa gag ctg Glu Asn Asn Lys Pro Pro Gln Ala Asp Ala Gly Pro Asp Lys Glu Leu 545 550 555			1824
acc ctg ccc gtg gac agc aca acc ctg gac ggc agc aag agc aca gat Thr Leu Pro Val Asp Ser Thr Thr Leu Asp Gly Ser Lys Ser Thr Asp 560 565 570 575			1872
gac cag aga gtc gtc tct tac ctt tgg gag cag agt cgg gga cct gac Asp Gln Arg Val Val Ser Tyr Leu Trp Glu Gln Ser Arg Gly Pro Asp 580 585 590			1920
ggg gtg cag ctg gag aat gcc aac agc agt gtc gcc act gtg act ggg Gly Val Gln Leu Glu Asn Ala Asn Ser Ser Val Ala Thr Val Thr Gly 595 600 605			1968
ctg caa gtc ggg act tat gta ttc acc ttg act gtc aaa gat gag agg Leu Gln Val Gly Thr Tyr Val Phe Thr Leu Thr Val Lys Asp Glu Arg 610 615 620			2016
aac cta cag agc cag agc tcc gtt aat gtc att gtc aaa gaa gaa ata Asn Leu Gln Ser Gln Ser Ser Val Asn Val Ile Val Lys Glu Glu Ile 625 630 635			2064
aac aaa ccg cca gta gcc aag atc gct ggg aac gtg gtg gtg acc ttg Asn Lys Pro Pro Val Ala Lys Ile Ala Gly Asn Val Val Val Thr Leu 640 645 650 655			2112
ccc acg agc aca gct gag ctg gat ggc tcg agg tcc tca gat gac aag Pro Thr Ser Thr Ala Glu Leu Asp Gly Ser Arg Ser Ser Asp Asp Lys 660 665 670			2160
ggg ata gtc agc tac ctg tgg act cga gat gag acg agc cca gcc gca Gly Ile Val Ser Tyr Leu Trp Thr Arg Asp Glu Thr Ser Pro Ala Ala 675 680 685			2208
ggg gag gtg ctg aat cac tct gac cac cac cct gtc ctc ttc ctc tcc Gly Glu Val Leu Asn His Ser Asp His His Pro Val Leu Phe Leu Ser 690 695 700			2256
aac ctg gtg gag ggg acc tac acg ttt cac ctg aaa gtg aca gat gca Asn Leu Val Glu Gly Thr Tyr Thr Phe His Leu Lys Val Thr Asp Ala 705 710 715			2304
aag ggc gag agc gac aca gac cgg acg aca gtg gaa gtg aag cct gac Lys Gly Glu Ser Asp Thr Asp Arg Thr Thr Val Glu Val Lys Pro Asp 720 725 730 735			2352

ccc agg aaa agc aac cta gtg gag atc atc ttg gat gtg aac gtc agt Pro Arg Lys Ser Asn Leu Val Glu Ile Ile Leu Asp Val Asn Val Ser 740 745 750	2400
cag ctg act gag agg ctg aag ggg atg ctc atc cgc cag att ggg gtc Gln Leu Thr Glu Arg Leu Lys Gly Met Leu Ile Arg Gln Ile Gly Val 755 760 765	2448
ctc ctg ggg gtg ctg gat tcc gac atc att gtg caa aag att cag ccg Leu Leu Gly Val Leu Asp Ser Asp Ile Ile Val Gln Lys Ile Gln Pro 770 775 780	2496
tac acg gag cag agc acc aag atg ttg ttt ttt gtt cag aac gac cct Tyr Thr Glu Gln Ser Thr Lys Met Leu Phe Phe Val Gln Asn Asp Pro 785 790 795	2544
ccc cac cag ctc ttc aaa ggc cat gag gtg gca gcc atg ctc aag agc Pro His Gln Leu Phe Lys Gly His Glu Val Ala Ala Met Leu Lys Ser 800 805 810 815	2592
gag ctg cag aag cag aag gct gac ttc ctc atc ttc aga gcc ctg gaa Glu Leu Gln Lys Gln Lys Ala Asp Phe Leu Ile Phe Arg Ala Leu Glu 820 825 830	2640
atc agc aca gtc aca tgt cag ctg aac tgt tct gac cat ggc cac tgt Ile Ser Thr Val Thr Cys Gln Leu Asn Cys Ser Asp His Gly His Cys 835 840 845	2688
gac tca ttc acc aag cgc tgt gtc tgt gac ccg ttt tgg atg gag aat Asp Ser Phe Thr Lys Arg Cys Val Cys Asp Pro Phe Trp Met Glu Asn 850 855 860	2736
ttc atc aag gtg cag ctg agg gat gga gac agc aac tgt gaa tgg agc Phe Ile Lys Val Gln Leu Arg Asp Gly Asp Ser Asn Cys Glu Trp Ser 865 870 875	2784
gtg ctc tac gtc atc att gcc tcc ttt gtc att gtt gtt gcc ttg ggg Val Leu Tyr Val Ile Ile Ala Ser Phe Val Ile Val Val Ala Leu Gly 880 885 890 895	2832
atc ctg tca tgg act aca atc tgc tgc tgc aag agg caa aaa gga aaa Ile Leu Ser Trp Thr Thr Ile Cys Cys Cys Lys Arg Gln Lys Gly Lys 900 905 910	2880
ccc aag agg aaa agc aga tac aag atc ctg gat gcc aca gat cag gag Pro Lys Arg Lys Ser Arg Tyr Lys Ile Leu Asp Ala Thr Asp Gln Glu 915 920 925	2928
agc ctg gag ctg aaa cca acc tcc cga gca ggc agc aaa cag aaa ggc Ser Leu Glu Leu Lys Pro Thr Ser Arg Ala Gly Ser Lys Gln Lys Gly 930 935 940	2976
ccc acg ctg agc agc agc ctg atg cat tct gaa tcg gag ctg gac agc Pro Thr Leu Ser Ser Ser Leu Met His Ser Glu Ser Glu Leu Asp Ser 945 950 955	3024

gac gat gcc atc ttc aca tgg cca gac cgg gag aag ggc aaa cta ctg 3072
 Asp Asp Ala Ile Phe Thr Trp Pro Asp Arg Glu Lys Gly Lys Leu Leu
 960 965 970 975

tat ggt cag aat ggc tct gtg cca aac ggg caa aca cct ttg aag tcc 3120
 Tyr Gly Gln Asn Gly Ser Val Pro Asn Gly Gln Thr Pro Leu Lys Ser
 980 985 990

agg agc gca cgg gag gag atc ttg tag 3147
 Arg Ser Ala Arg Glu Glu Ile Leu
 995

<210> 22
 <211> 1048
 <212> PRT
 <213> Mus musculus

<400> 22

Met Glu Lys Arg Leu Gly Val Lys Pro Ser Pro Ala Ser Trp Val Leu
 -45 -40 -35

Pro Gly Tyr Cys Trp Gln Thr Ser Val Lys Leu Pro Arg Ser Leu Tyr
 -30 -25 -20

Leu Leu Tyr Ser Phe Phe Cys Phe Ser Val Leu Trp Leu Ser Thr Asp
 -15 -10 -5

Ala Asp Glu Ser Arg Cys Gln Gln Gly Lys Thr Leu Tyr Gly Ala Gly
 -1 1 5 10 15

Leu Arg Thr Glu Gly Glu Asn His Leu Arg Leu Leu Ala Gly Ser Leu
 20 25 30

Pro Phe His Ala Cys Arg Ala Ala Cys Cys Arg Asp Ser Ala Cys His
 35 40 45

Ala Leu Trp Trp Leu Glu Gly Met Cys Phe Gln Ala Asp Cys Ser Lys
 50 55 60

Pro Gln Ser Cys Gln Pro Phe Arg Thr Asp Ser Ser Asn Ser Met Leu
 65 70 75

Ile Ile Phe Gln Lys Ser Gln Thr Thr Asp Asp Leu Gly Leu Leu Pro
 80 85 90 95

Glu Asp Asp Glu Pro His Leu Leu Arg Leu Gly Trp Gly Arg Thr Ser

100										105					110				
Trp	Arg	Arg	Gln	Ser	Leu	Leu	Gly	Ala	Pro	Leu	Thr	Leu	Ser	Val	Pro				
			115					120					125						
Ser	Ser	His	His	Gln	Ser	Leu	Leu	Arg	Asp	Arg	Gln	Lys	Arg	Asp	Leu				
		130					135					140							
Ser	Val	Val	Pro	Thr	His	Gly	Ala	Met	Gln	His	Ser	Lys	Val	Asn	His				
	145					150					155								
Ser	Glu	Glu	Ala	Gly	Ala	Leu	Ser	Pro	Thr	Ser	Ala	Glu	Val	Arg	Lys				
160					165					170					175				
Thr	Ile	Thr	Val	Ala	Gly	Ser	Phe	Thr	Ser	Asn	His	Thr	Thr	Gln	Thr				
			180						185					190					
Pro	Glu	Trp	Pro	Lys	Asn	Val	Ser	Ile	His	Pro	Glu	Pro	Ser	Glu	His				
			195					200					205						
Ser	Ser	Pro	Val	Ser	Gly	Thr	Pro	Gln	Val	Lys	Ser	Thr	Glu	His	Ser				
		210					215					220							
Pro	Thr	Asp	Ala	Pro	Leu	Pro	Val	Ala	Pro	Ser	Tyr	Ser	Tyr	Ala	Thr				
	225					230					235								
Pro	Thr	Pro	Gln	Ala	Ser	Ser	Gln	Ser	Thr	Ser	Ala	Pro	His	Pro	Val				
240					245					250					255				
Val	Lys	Glu	Leu	Val	Val	Ser	Ala	Gly	Lys	Ser	Val	Gln	Ile	Thr	Leu				
			260						265					270					
Pro	Lys	Asn	Glu	Val	Gln	Leu	Asn	Ala	Phe	Val	Leu	Pro	Glu	Ala	Glu				
		275						280					285						
Pro	Gly	Glu	Thr	Tyr	Thr	Tyr	Asp	Trp	Gln	Leu	Ile	Thr	His	Pro	Thr				
	290						295					300							
Asp	Tyr	Ser	Gly	Glu	Val	Glu	Arg	Lys	His	Ser	Gln	Ser	Leu	Gln	Leu				
	305					310					315								
Ser	Lys	Leu	Thr	Pro	Gly	Leu	Tyr	Glu	Phe	Lys	Val	Thr	Val	Asp	Gly				
320					325					330					335				

Gln Asn Ala His Gly Glu Gly Tyr Val Asn Val Thr Val Lys Pro Glu
 340 345 350

Pro Arg Lys Asn Arg Pro Pro Val Ala Val Val Ser Pro Gln Phe Gln
 355 360 365

Glu Ile Ser Leu Pro Thr Thr Ser Thr Ile Ile Asp Gly Ser Gln Ser
 370 375 380

Thr Asp Asp Asp Lys Ile Val Gln Tyr His Trp Glu Glu Leu Lys Gly
 385 390 395

Pro Leu Arg Glu Glu Lys Ile Ser Glu Asp Thr Ala Ile Leu Lys Leu
 400 405 410 415

Ser Lys Leu Val Pro Gly Asn Tyr Thr Phe Ser Leu Thr Val Val Asp
 420 425 430

Ser Asp Gly Ala Thr Asn Ser Thr Thr Ala Ser Leu Thr Val Asn Lys
 435 440 445

Ala Val Asp Tyr Pro Pro Val Ala Asn Ala Gly Pro Asn Gln Val Ile
 450 455 460

Thr Leu Pro Gln Asn Ser Ile Thr Leu Phe Gly Asn Gln Ser Thr Asp
 465 470 475

Asp His Gly Ile Thr Ser Tyr Glu Trp Ser Leu Ser Pro Ser Ser Lys
 480 485 490 495

Gly Lys Val Val Glu Met Gln Gly Val Arg Thr Pro Ala Leu Gln Leu
 500 505 510

Ser Ala Met Gln Glu Gly Asp Tyr Thr Tyr Gln Leu Thr Val Thr Asp
 515 520 525

Thr Ala Gly Gln Gln Ala Thr Ala Gln Val Thr Val Ile Val Gln Pro
 530 535 540

Glu Asn Asn Lys Pro Pro Gln Ala Asp Ala Gly Pro Asp Lys Glu Leu
 545 550 555

Thr Leu Pro Val Asp Ser Thr Thr Leu Asp Gly Ser Lys Ser Thr Asp
 560 565 570 575

Asp Gln Arg Val Val Ser Tyr Leu Trp Glu Gln Ser Arg Gly Pro Asp
 580 585 590

Gly Val Gln Leu Glu Asn Ala Asn Ser Ser Val Ala Thr Val Thr Gly
 595 600 605

Leu Gln Val Gly Thr Tyr Val Phe Thr Leu Thr Val Lys Asp Glu Arg
 610 615 620

Asn Leu Gln Ser Gln Ser Ser Val Asn Val Ile Val Lys Glu Glu Ile
 625 630 635

Asn Lys Pro Pro Val Ala Lys Ile Ala Gly Asn Val Val Val Thr Leu
 640 645 650 655

Pro Thr Ser Thr Ala Glu Leu Asp Gly Ser Arg Ser Ser Asp Asp Lys
 660 665 670

Gly Ile Val Ser Tyr Leu Trp Thr Arg Asp Glu Thr Ser Pro Ala Ala
 675 680 685

Gly Glu Val Leu Asn His Ser Asp His His Pro Val Leu Phe Leu Ser
 690 695 700

Asn Leu Val Glu Gly Thr Tyr Thr Phe His Leu Lys Val Thr Asp Ala
 705 710 715

Lys Gly Glu Ser Asp Thr Asp Arg Thr Thr Val Glu Val Lys Pro Asp
 720 725 730 735

Pro Arg Lys Ser Asn Leu Val Glu Ile Ile Leu Asp Val Asn Val Ser
 740 745 750

Gln Leu Thr Glu Arg Leu Lys Gly Met Leu Ile Arg Gln Ile Gly Val
 755 760 765

Leu Leu Gly Val Leu Asp Ser Asp Ile Ile Val Gln Lys Ile Gln Pro
 770 775 780

Tyr Thr Glu Gln Ser Thr Lys Met Leu Phe Phe Val Gln Asn Asp Pro
785 790 795

Pro His Gln Leu Phe Lys Gly His Glu Val Ala Ala Met Leu Lys Ser
800 805 810 815

Glu Leu Gln Lys Gln Lys Ala Asp Phe Leu Ile Phe Arg Ala Leu Glu
820 825 830

Ile Ser Thr Val Thr Cys Gln Leu Asn Cys Ser Asp His Gly His Cys
835 840 845

Asp Ser Phe Thr Lys Arg Cys Val Cys Asp Pro Phe Trp Met Glu Asn
850 855 860

Phe Ile Lys Val Gln Leu Arg Asp Gly Asp Ser Asn Cys Glu Trp Ser
865 870 875

Val Leu Tyr Val Ile Ile Ala Ser Phe Val Ile Val Val Ala Leu Gly
880 885 890 895

Ile Leu Ser Trp Thr Thr Ile Cys Cys Cys Lys Arg Gln Lys Gly Lys
900 905 910

Pro Lys Arg Lys Ser Arg Tyr Lys Ile Leu Asp Ala Thr Asp Gln Glu
915 920 925

Ser Leu Glu Leu Lys Pro Thr Ser Arg Ala Gly Ser Lys Gln Lys Gly
930 935 940

Pro Thr Leu Ser Ser Ser Leu Met His Ser Glu Ser Glu Leu Asp Ser
945 950 955

Asp Asp Ala Ile Phe Thr Trp Pro Asp Arg Glu Lys Gly Lys Leu Leu
960 965 970 975

Tyr Gly Gln Asn Gly Ser Val Pro Asn Gly Gln Thr Pro Leu Lys Ser
980 985 990

Arg Ser Ala Arg Glu Glu Ile Leu
995

<210> 23

<211> 691
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (633)..(633)
 <223> 'n' stands for unidentified base.

<220>
 <221> misc_feature
 <222> (680)..(680)
 <223> 'n' stands for unidentified base.

<220>
 <221> misc_feature
 <222> (682)..(682)
 <223> 'n' stands for unidentified base.

<400> 23
 ccggcgctccg gcagatgcac gcggggcggg ggccggggga gaggcgggga gagagaaccc 60
 acaacaaaac ttggctcgct gcgcccacgg ctcgacttga atgacaggag ccggcgcccc 120
 cggagcgcag cggacacccg cgagcctgtt ccgcccacgg cgcggcgcgc agcggcaggt 180
 gctggcaagg gccagtggca tcagatcccc cagagctggg gttacagggtg gttgtgagtc 240
 atcccagaga gtgctgggct cagtcttctg tgagcagagc actgctctta acagataagc 300
 ttgtggactt ttatggagac aagccaaagg tgagagaaga aagccagcct gtccagcacc 360
 atggctggca gcaggggcct gccactccta ctgctgggtgc ttcagctctt cctggggcct 420
 gtgctgcctg tgagggcacc tgtgtttggc cgaagtgaca cccccaccct gagccccgag 480
 gagaatgaat ttgtggagga agagaatcag ccagtgtctg ttctgagctc cgaggagcca 540
 gagcctggcc agccactgtc gactgtcccg agattgggtgc ctgttccagg aaggtgtatg 600
 gactgtggtg gcattgacct gcgtgagttt cangggaact gccgagcaca ccaaccatct 660
 tctcttgtag aaaaaccagn tngagaaaat c 691

<210> 24
 <211> 572
 <212> DNA
 <213> Mus musculus

<400> 24
 gctgctgtca ggtgggtccct tttatgggtg gttcctgtgg tcgctgcgca gcggctggcc 60
 gacttccgca gcgggtctcg ggccaccgag cgccgtcttc acccagcgcc atggctgtgg 120

ccgctgtcgg ccgcccgaga gccctgcgct gcccgtgtt gtcctgtctg tcactcctgc	180
tggtagccgg ccctgcgctg ggctggaacg accctgacag aatactcttg 'cgggatgtga	240
aagctcttac cctctactcc gaccgctaca ccacctcccg gaggctggac cctatccac	300
agttgaagtg tgttggaggc accgccggtt gtgaggccta tccccccagg gtgatacagt	360
gccagaacaa aggctgggat ggctacgatg tacagtggga atgtaagacc gacttggata	420
ttgcatacaa atttggcaaa actgtggtga gctgtgaagg ctacgagtcc tctgaagacc	480
agtatgtcct caggggttcc tgcggcttgg agtacaactt agattacaca gagctgggcc	540
tgaagaaact gaaggagcgc ggccgcgtcg ac	572

<210> 25
 <211> 877
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (662)..(662)
 <223> 'n' stands for unidentified base.

<400> 25	
ctccgccgca gttctcggtg ggtcgccggg cagccctccc gccatgcacc tgctgcttgc	60
agccgcgttc gggctgctgc tgctgctgcc gccgccggg gccgtagcct cccggaagcc	120
gacgatgtgc cagagatgcc ggacgctggt ggacaagtgc aaccagggga tggccaacac	180
ggccaggaag aatttcggtg gcggcaacac ggcgtgggaa gagaagacgc tgtctaagta	240
cgaattcagt gagatccggc ttctggagat catggagggg ctgtgtgaca gcagtgactt	300
tgagtgaac caactcttgg agcagcagga ggagcagcta gaggcttggg ggcagacact	360
gaagaaggag caccccaacc tatttgagtg gttctgtgta cacacactga aagcgtgctg	420
tcttccaggc acctacgggc cagactgtca agagtgccag ggtgggtccg agaggccttg	480
cagcggaaac ggctattgca gcggagacgg cagcagacag ggcgacgggt cctgccagtg	540
tcacacaggc tacaaggac cactgtgtat tgactgcaca gacggcttct tcagcttgca	600
gaggaacgag acccacagca tctgctcagc ctgtgatgag tcttgcaaga cctgctctgg	660
tncaagcaac aaagactgta tccagtgtga agtgggctgg gcacgtgtgg aggatgcctg	720
tgtggatgtg gatgagtgtg cagcagagac atctccgtgc agcgatggcc agtactgtga	780
gaatgtcaac ggctcgtaca catgtgaaga ctgtgattct acctgcgtgg gctgtacagg	840

aaaaggccca gccaaactgta aggagtgtat tgccggc 877

<210> 26
 <211> 930
 <212> DNA
 <213> Mus musculus

<400> 26
 aggggacccg cggcacgagc gagagctcgc cagccccgcc acgatgcccc cgcgcccagg 60
 acgcctcctc cagccgctgg ccgggctgcc ggccctggcc acgctcctgc tgctgctcgg 120
 ggcgcgcaaa ggcgcccggg cccaggaggt ggaagcggac agcggggtcg agcaggaccc 180
 gcacgccaag cacctgtata cggccgacat gttcacgcac gggatccaga gcgccgcgca 240
 ctctgcatg ttcttcgcgc cctgggtgtg aactgccag cggctgcagc caacttgaa 300
 tgacctggga gacaagtaca acagcatgga ggatgccaag gtctacgtgg ccaaagtga 360
 ctgcacggct gattccgacg tgtgctctgc ccagggagtg cgaggatacc ccaccctgaa 420
 gttttttaag cctggacaag aagcagtga gtaccagggt cctagagact ttgaaacact 480
 ggaaaactgg atgctgcaga cactgaacga ggagccagcc acaccggagc cggaagcgga 540
 accaccaga gccctgagc tcaaacaggg gttgtatgag ctctcgcca acaactttga 600
 gctgcatgtt tctcaaggca accactttat caagttcttc gtcctgtggt gcggtcactg 660
 caaagctctg gctccaacct gggagcagct ggctctgggc cttgaacatt ctgaaaccgt 720
 caagattggc aaggttgact gcacgcagca ctacgctgtc tgctcagagc atcaggtcag 780
 aggctatcca actctgctct ggtttcgaga tggcaagaag gtggatcagt acaagggaaa 840
 gcgggacttg gagtcaactga gagactatgt gcagtcccag ctgcagggtt cagaggcagc 900
 tccggagact gttgagccgt cagaggcccc 930

<210> 27
 <211> 641
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (325)..(325)
 <223> 'n' stands for unidentified base.

<220>
 <221> misc_feature
 <222> (329)..(329)

<223> 'n' stands for unidentified base.

<400> 27

```

aggggaggga cggggcgggt tgcggagggt aggcacgcgg aggccggggc atgcgtgcgg      60
gccggtgtgc cgcggcgctg ctgctgctgc tactgagcgg cgcggggcgc gcgatcggct      120
ccgaggacat cgtggtaggc tgcggggggt tcgtgaagtc ggacgtggag atcaactact      180
cgctcatcga gataaagtta tacaccaagc atgggacttt gaaatatcag acggactgtg      240
ctcctaacaa cggctacttt atgatcccct tgtatgataa gggggatttc atcctgaaga      300
tcgaacctcc tctgggctgg agttntganc caaccaacgt gtagctgcga gtggatgggt      360
tgagcgacat ctgcacgaag ggcggggaca tcaacttcct attcactggc ttctctgtga      420
atggcaaggt cctcagcaaa ggcagcccc tgggcccagc aggagttagc gtatccctga      480
gaagcaccgg tgctgactcg aagatccagt ctacagtcac gcagcctggc ggaaagttag      540
cgtttttcca agttcttcct ggagattatg aaatccttgc aactcaccgc acctgggccc      600
tgaaggaggc aagtaccacg gtgcgtgtga cgaactcgaa t                          641

```

<210> 28

<211> 703

<212> DNA

<213> Mus musculus

<400> 28

```

gcgcgtgcgc gacccccgcc tgggcctcca gtgggacagc ctccctgggg gctttggcag      60
gtgtcacttc ttcaccttgg cgtcataagg gcctgcgttt ttgtaggcac tcacgtagcc      120
actgtcgtcc aggatgtcct gccgtccagc gatgcccttt cccttgccgc tctcatcaaa      180
gcgttctttg tgggagcccg tatacttact ggtgtcgcgc agccggtcca cagcaccacc      240
cgtttttagct ttggtgacgc caatgttggc cggttccttg cccgctatca gctggcagat      300
ggcatcaaag gcctcctcct tggacttccc cttgaaccgc ttagttgcca gctcttcag      360
ggccttcttg aactcctcat agttgattac tctagcagat ttgccttga ctttggagaa      420
gacgatgtcg acgtcgggtc ccgttacggc ctttcgctcg gccaccttac agtccttgca      480
cagcttggcc cagttcttgc cattcatctc ttgcccgctg gccttggggg cgccatggat      540
ggcaaacttc cggaagctct cctccagccc agctatgtcc gtgctcgtcg ccatgccacc      600
cggcttctac cgcttggctg ctccctgagcg tgccttcgga caggacccag gaactgatgc      660
tggagaccag gaggtccac agctccgctc cctgccgggt ccc                          703

```

<210> 29
 <211> 934
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (605)..(605)
 <223> 'n' stands for unidentified base.

<400> 29
 ccgaggttca agaggagcct agggagtgcc agctctcgct gaccggcggg tcccagagac 60
 ctgcccccaa ggtgtccac tgtgtggcta aggggtgggat agaaccggg ctgggagagc 120
 cgggttatgg gttccagtgg tggttccgcc gcttccttgc ttcgctctgt cttacctcgg 180
 cgttcagcct atttttcctc gtaagaattg gacacttttc cgtgcccctt ccataccgca 240
 ggtggtgttc gtagaggctc tcacgctttt caaaaggcgt ctcatctaag acttgctaga 300
 accaacctga ctaaaggagt caccgtcata ccccccttgc acctggagta aatctgactg 360
 tccgaaggac gaaggaccgg tctgtgagca cttgtgctaa ggtggacttt attcacactc 420
 ctgagtggaat tattatttgt cactcactcc tgagtcctgc cgtttggagg ggctgccttt 480
 ggaaatgagt tctgggaact gaacacagga actgggtgcc tgtaccaggc ttgccatttg 540
 cctgaccgag ttactcttct ttggatcccg gcgctgcagt acttttgaat tgttcctgtg 600
 aaggncagaa gtaggtattt ggtcccttgg agctgtgagc tgatgtaggt gctgggaact 660
 cagctgtggg gtgctgcaag accaaggacg agtcttgcag tgttaagtgt tttcctcagg 720
 gtgctcagac ggtgaaaatc agagatcagg ccacctttct gtgagccttc agctgagtct 780
 aaagggtgta ttgatcagaa tggcttcagg atgggttttac ctgtcctgca tgggtgctggg 840
 atcgctggga tcgatgtgca tcctcttcac tgctactgg atgcagtact ggcgcggtgg 900
 ctttgccctgg gatggcacgg tgctcatgtt taac 934

<210> 30
 <211> 812
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (589)..(589)
 <223> 'n' stands for unidentified base.

<400> 30
ggaggctgag gcaagaggga gctgtccggg tggggagcca gcatttcctt cttcctcctc 60
tgcgtgaggg gagagaaggt tgggggtccc cgagcccatg gatcgggagg aggcggaggc 120
cgccgagagc cggcaccctt ctatgtggcc ctgagccccg tgtactgggt cgcctctctt 180
ggaaggccat ggagaagaga ctgggagtca agccaagtcc cgcttcctgg gttttgccag 240
gatattgttg gcagacatca gtgaagctgc cgagaagcct gtacctgctt tacagtttct 300
tctgcttcag cgttctgtgg ttgtcaacag atgctgatga gagcagatgc caacagggga 360
agacacttta tggagctggc ttgagaactg agggagaaaa tcacctccgg cttcttgagc 420
gaagcctgcc tttccacgcc tgtcgggctg cctgctgccg ggactctgcc tgccacgctc 480
tatggtggct ggaagggatg tgctttcagg ctgactgcag taagccccag agctgccagc 540
cttttaggac agactcttcc aattccatgc tgatcatttt tcaaaaatnc caaactacag 600
atgatttggg ccttctgcct gaagatgatg aaccacatct tctgaggcta ggctggggca 660
ggacatcgtg gaggaggcag agccttcttg gggctcccct caccctttct gtaccctcta 720
gtcaccacca gagcttactc agggatcggc agaagagaga tctcagtgtg gtacctacac 780
atggagcgtg gcagcattct aaagtgaatc ac 812

<210> 31
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide designed to act as primer for amplifying cDNA fragment of secretory or membrane proteins derived from mouse white adipose tissue.

<400> 31
gggggtggac catcctcta 19

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide designed to act as primer for amplifying cDNA fragment of secretory or membrane proteins derived from mouse white adipose tissue.

<400> 32
cgcgagctg taaacggtag 20

<210> 33
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide designed to act as 5'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST20-14.

 <400> 33
 caggcccctg ctgccagcca t 21

 <210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide designed to act as 3'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST20-14.

 <400> 34
 atgcacgcgg ggcggggggcc 20

 <210> 35
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide designed to act as 5'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST22-22.

 <400> 35
 gcgaccacag gaacccacca t 21

 <210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide designed to act as 3'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST22-22.

 <400> 36
 atggtggggtt cctgtggtcg 20

 <210> 37
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as 5'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST8-5.

<400> 37
 ggctgcaagc agcaggtgca t 21

<210> 38
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as 3'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST8-5.

<400> 38
 atgcacctgc tgcttgacgc 20

<210> 39
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as 5'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST19-15.

<400> 39
 gcgtcctggg cgcggggggca t 21

<210> 40
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as 3'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST19-15.

<400> 40
 atgccccgc gccagacg 20

<210> 41
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as 5'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST13-11.

<400> 41
 ggcacaccgg cccgcacgca t 21

<210> 42
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as 3'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST13-11.

<400> 42
 atgcgtgcgg gccggtgtgc 20

<210> 43
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as 5'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST9-8.

<400> 43
 tatgtccgtg ctcgctgcca t 21

<210> 44
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as 3'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST9-8.

<400> 44
 atgtcctgcc gtccagcgat 20

<210> 45
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide designed to act as 5'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST21-3.

<400> 45
 gtaaaaccat cctgaagcca t 21

<210> 46

<211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide designed to act as 3'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST21-3.

 <400> 46
 atgggttcca gtggtggttc 20

 <210> 47
 <211> 21
 <212> DNA
 <213> Artificial Sequece

 <220>
 <223> Oligonucleotide designed to act as 5'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST20-6.

 <400> 47
 gactcccgagt ctcttctcca t 21

 <210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide designed to act as 3'-RACE gene-specific primer f
 or identifying base sequence encoding full length mSST20-6.

 <400> 48
 atggatcggg aggaggcgga 20